88796

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From: Jiang, Dong
Sent: Tuesday, March 11, 2003 6:40 PM
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Subject: 09/636,530

Priority = ED = 8/10/00
Cantor, T.

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(STIC)

Please search SEQ ID NO:2 and 3

-issued & publ.
-commercial

Please send results on paper to Dong Jiang in 10D-08 (mail stop CM1-10D19).
Thank you very much.

Dong Jiang (78243)
703-305-1345
U.S. Patent and Trademark Office
Art Unit 1646
dong.jiang@uspto.gov
CM1-10D08
Mail stop: CM1-10D19

Edward Hart
Technical Info. Specialist
STIC/Biotech
CMI 6B02 Tel: 305-9203

Searcher:
Phone:
Location:
Date Picked Up: 3/13/03
Date Completed: 3/14/03
Searcher Prep/Review:
Clerical:
Online time:

TYPE OF SEARCH:
NA Sequences:
AA Sequences: 2
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

VENDOR/COST (where applic.)
STN:
DIALOG:
Questel/Orbit:
DRLink:
Lexis/Nexis:
Sequence Sys.: EDH
WWW/Internet:
Other (specify):

BioTech-Chem Library
Search Results
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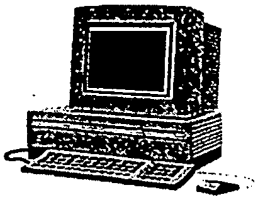

Scientific & Technical Information C

The search results generated for your recent request are attached. If you have any questions or comme (compliments or complaints) about the scope or the results of the search, please contact *the BioTech-C searcher* who conducted the search *or contact*:

Mary Hale, Supervisor, 308-4
CM-1 Room 1E01

Voluntary Results Feedback Form

- *I am an examiner in Workgroup:* *(Example: 1610)*
- *Relevant prior art* ***found****, search results used as follows:*
  - ☐ 102 rejection
  - ☐ 103 rejection
  - ☐ Cited as being of interest.
  - ☐ Helped examiner better understand the invention.
  - ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
  (journal articles, conference proceedings, new product announcements etc.)

- *Relevant prior art* ***not found****:*
  - ☐ Results verified the lack of relevant prior art (helped determine patentability).
  - ☐ Search results were not useful in determining patentability or understanding the invent

Other Comments:

Drop off completed forms at the **Circulation Desk CM-1**, or send to Mary Hale, **CM1-1E01 or mary.hale@uspto.gov**

```
KW   bone formation; osteoporosis; hypoparathyroidism; hypertension;
KW   climacteric disturbance.
XX
OS   Synthetic.
XX
PN   EP748817-A2.
XX
PD   18-DEC-1996.
XX
PF   13-JUN-1996;   96EP-0109475.
XX
PR   15-JUN-1995;   95JP-0148652.
XX
PA   (TAKE ) TAKEDA CHEM IND LTD.
XX
PI   Fukuda T,  Habashita J,  Nakagawa S,  Taketomi S;
XX
DR   WPI; 1997-036114/04.
XX
PT   New parathyroid hormone derivs.  - useful in treatment of bone
PT   diseases, hypoparathyroidism and hypertension
XX
PS   Claim 3; Page 39; 42pp; English.
XX
CC   The sequences given in AAW08103-07 represent fragments of human para-
CC   thyroid hormone (PTH) which were used as Xaa34 in the generic sequence
CC   given in AAW08102.  Peptides based on the generic sequence are human PTH
CC   (1-34) derivative peptides. They have potent cAMP-producing activity and
CC   bone formation activity.  They may be used in treatment of bone
CC   diseases including osteoporosis, hypoparathyroidism, hypertension
CC   and climacteric disturbance.  The peptides are low in toxicity and
CC   are safe.
XX
SQ   Sequence   51 AA;

  Query Match             98.0%;  Score 248;  DB 18;  Length 51;
  Best Local Similarity   98.0%;  Pred. No. 3.8e-26;
  Matches   50;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
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Db          1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEADKADVNVLTKAKSQ 51


RESULT 5
AAR11732
ID   AAR11732 standard; Protein; 55 AA.
XX
AC   AAR11732;
XX
DT   03-JUL-1991  (first entry)
XX
DE   PTH-(29-84).
XX
KW   Parathyroid hormone; calcium; osteoporosis; bone.
XX
OS   Synthetic.
XX
PN   WO9105050-A.
XX
PD   18-APR-1991.
XX
PF   01-OCT-1990;   90WO-C000335.
XX
PR   29-SEP-1989;   89CA-2615001.
XX
PA   (CANA ) NAT RES COUNCIL CAN.
XX
PI   Sung WL;
XX
DR   WPI; 1991-132857/18.
DR   N-PSDB; AAQ11618.
XX
```

```
PT   Mature human parathyroid synthesis - includes using eg E. coli
PT   transformed by plasmid contg. synthetic nucleotide sequence contg.
PT   adenine rich codons in N-terminal region.
XX
PS   Disclosure; Fig 6; 62pp; English.
XX
CC   Codons 29-84 are degenerate in the usage frequency favoured by
CC   E.coli or yeast. Codons 1-28 (see AAQ11617) are designed to contain
CC   adenine rich codons. The sequence is  prepd. from eight oligo-
CC   nucleotides (4 on each strand). A plasmid contg. the complete
CC   sequence expresses PTH with an improved yield. PTH is a blood
CC   calcium regulator known to increase bone mass.
XX
SQ   Sequence   55 AA;

  Query Match             98.0%;  Score 248;  DB 12;  Length 55;
  Best Local Similarity   98.0%;  Pred. No. 4.2e-26;
  Matches   50;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
              |||||||||||||||||||||||||||||||||||||:|||||||||||||
Db          5 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEADKADVNVLTKAKSQ 55


RESULT 6
AAR30852
ID   AAR30852 standard; Protein; 78 AA.
XX
AC   AAR30852;
XX
DT   09-JUN-1993  (first entry)
XX
DE   hPTH mutein lacking 6 N-terminal amino acids.
XX
KW   Human parathyroid hormone; hPTH; antagonist; hypoparathyroidism;
KW   hypercalcaemia.
XX
OS   Synthetic.
XX
PN   EP528271-A.
XX
PD   24-FEB-1993.
XX
PF   05-AUG-1992;   92EP-0113322.
XX
PR   07-AUG-1991;   91JP-0198056.
PR   26-JUN-1992;   92JP-0169713.
XX
PA   (TAKE ) TAKEDA CHEM IND LTD.
XX
PI   Fukuda T;
XX
DR   WPI; 1993-060187/08.
DR   N-PSDB; AAQ35228.
XX
PT   New human parathyroid mutein(s) - useful for treating e.g.
PT   osteoporosis, hypoparathyroidism, hyperparathyroidism,
PT   hypercalcaemia, hypertension etc.
XX
PS   Disclosure; Page 7; 88pp; English.
XX
CC   The sequence is that of a human parathyroid hormone (hPTH) peptide
CC   lacking 6 hPTH N-terminal amino acids. The peptide can have higher
CC   stability, enhanced activity and improved absorption by tissues.
CC   It can act as a PTH antagonist and can be used as a therapeutic
CC   agent for hypercalcaemia and hyperparathyroidism.
XX
SQ   Sequence   78 AA;

  Query Match             98.0%;  Score 248;  DB 14;  Length 78;
  Best Local Similarity   98.0%;  Pred. No. 6.5e-26;
  Matches   50;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;
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Db      28 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEADKADVNVLTKAKSQ 78


RESULT 7
AAR30859
ID   AAR30859 standard; Protein; 78 AA.
XX
AC   AAR30859;
XX
DT   09-JUN-1993  (first entry)
XX
DE   Leu8 hPTH (7-84) mutein.
XX
KW   Human parathyroid hormone; hPTH; antagonist; hypoparathyroidism;
KW   hypercalcaemia.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Region          2
FT                   /note= "Met -> Leu"
XX
PN   EP528271-A.
XX
PD   24-FEB-1993.
XX
PF   05-AUG-1992;    92EP-0113322.
XX
PR   07-AUG-1991;    91JP-0198056.
PR   26-JUN-1992;    92JP-0169713.
XX
PA   (TAKE ) TAKEDA CHEM IND LTD.
XX
PI   Fukuda T;
XX
DR   WPI; 1993-060187/08.
DR   N-PSDB; AAQ36836.
XX
PT   New human parathyroid mutein(s) - useful for treating e.g.
PT   osteoporosis, hypoparathyroidism, hyperparathyroidism,
PT   hypercalcaemia, hypertension etc..
XX
PS   Example; Page 22; 88pp; English.
XX
CC   The sequence is that of mutated human parathyroid hormone (hPTH)
CC   (7-84) where Met8 is substd. by Leu. It has higher stability, enhanced
CC   activity and improved absorption by tissues. It can act as a PTH
CC   antagonist and can be used as a therapeutic agent for hypercalcaemia
CC   and hyperparathyroidism.
XX
SQ   Sequence   78 AA;

  Query Match             98.0%;  Score 248;  DB 14;  Length 78;
  Best Local Similarity   98.0%;  Pred. No. 6.5e-26;
  Matches   50;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
             |||||||||||||||||||||||||||||||||||||:|||||||||||||
Db      28 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEADKADVNVLTKAKSQ 78


RESULT 8
AAE23725
ID   AAE23725 standard; peptide; 78 AA.
XX
AC   AAE23725;
XX
DT   10-SEP-2002  (first entry)
XX
DE   Human parathyroid hormone (hPTH) peptide (7-84).
XX
KW   Human parathyroid hormone; hPTH; PTH-related peptide; PTHrP; eczema;
KW   hyperproliferative skin disorder; psoriasis; ichthyosis; skin cancer;
KW   acne; actinic keratosis; alopecia; gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO200228420-A2.
XX
PD   11-APR-2002.
XX
PF   05-OCT-2001; 2001WO-US31082.
XX
PR   06-OCT-2000; 2000US-238134P.
XX
PA   (HOLI/) HOLICK M F.
XX
PI   Holick MF;
XX
DR   WPI; 2002-452304/48.
DR   N-PSDB; AAD37995.
XX
PT   Regulating mammalian skin or hair cell proliferation and
PT   differentiation by administering nucleic acids encoding peptides
PT   derived from N-terminal region of human parathyroid hormone (hPTH) or
PT   hPTH-related protein  -
XX
PS   Claim 35; Fig 15; 56pp; English.
XX
CC   The invention relates to a method for regulating proliferation or
CC   enhancing differentiation of mammalian skin or hair cell. The method
CC   involves administering nucleic acids encoding peptides derived from
CC   N-terminal region of human parathyroid hormone (hPTH) or hPTH-related
CC   peptide (PTHrP). The method is used for inhibiting hyperproliferative
CC   skin disorders such as psoriasis, ichthyosis, eczema, acne, actinic
CC   keratosis, skin cancer, for inhibiting hair growth or preventing hair
CC   regrowth. It is useful for stimulating cell growth, rejuvenating aged
CC   skin, preventing skin wrinkles, treating skin wrinkles, enhancing wound
CC   healing, stimulating hair growth, maintaining hair growth, treating or
CC   preventing female or male pattern baldness, for treating chemotherapy
CC   induced alopecia and also for stimulating epidermal cell growth or
CC   hair follicle cell growth. The method is also used in gene therapy.
CC   The present sequence is hPTH peptide.
XX
SQ   Sequence   78 AA;

  Query Match             98.0%;  Score 248;  DB 23;  Length 78;
  Best Local Similarity   98.0%;  Pred. No. 6.5e-26;
  Matches   50;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
             |||||||||||||||||||||||||||||||||||||:|||||||||||||
Db      28 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEADKADVNVLTKAKSQ 78


RESULT 9
AAU73024
ID   AAU73024 standard; Peptide; 78 AA.
XX
AC   AAU73024;
XX
DT   12-MAR-2002  (first entry)
XX
DE   Parathyroid hormone PTH/PTHrP modulating domain #6.
XX
KW   Human; parathyroid hormone; PTH; parathyroid hormone-related protein;
KW   PTHrP; bone resorption inhibitor; osteoprotegrin; OPG; OPG-L antibody;
KW   calcitonin; bisphosphonate; oestrogen; oestrogen receptor; tibolone;
KW   osteopenia; hyperthyroidism; hypercalcaemia; tumour metastasis; bone;
KW   breast cancer; prostate cancer; cachexia; anorexia; osteoporosis;
KW   Paget's disease; osteomyelitis; osteonecrosis; bone cell death;
KW   Gaucher's disease; sickle cell anaemia; systemic lupus erythematosus;
KW   rheumatoid arthritis; periodontal disease; alopecia; fracture repair;
KW   immunoglobulin G; IgG.
```

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                    GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on:         March 13, 2003, 14:46:09 ; Search time 8.75373 Seconds
                                           (without alignments)
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Title:          US-09-636-530-3
Perfect score:  253
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Scoring table:  BLOSUM62
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Searched:       262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters:      262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Issued_Patents_AA:*
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                2:  /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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                6:  /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                 SUMMARIES
                  %
Result          Query
  No.   Score   Match Length DB  ID .                      Description
-------------------------------------------------------------------------------
    1     248    98.0     51  3  US-09-044-536A-7          Sequence 7, Appli
    2     248    98.0     84  1  US-07-863-014-2           Sequence 2, Appli
    3     248    98.0     84  1  US-08-332-453-2           Sequence 2, Appli
    4     248    98.0     84  1  US-08-689-190-2           Sequence 2, Appli
    5     248    98.0     84  2  US-08-835-231-9           Sequence 9, Appli
    6     248    98.0     84  2  US-08-805-918-3           Sequence 3, Appli
    7     248    98.0     84  3  US-09-044-536A-36         Sequence 36, Appl
    8     248    98.0     84  4  US-09-108-661-9           Sequence 9, Appli
    9     248    98.0     84  5  PCT-US95-15800-25         Sequence 25, Appl
   10     243    96.0     84  2  US-08-142-551B-1          Sequence 1, Appli
   11     243    96.0     84  2  US-08-411-726-1           Sequence 1, Appli
   12     238    94.1     84  1  US-07-707-114-1           Sequence 1, Appli
   13     237    93.7     50  2  US-08-142-551B-119        Sequence 119, App
   14     209    82.6     78  2  US-08-733-446-1           Sequence 1, Appli
   15     209    82.6     79  2  US-08-733-446-2           Sequence 2, Appli
   16     209    82.6     80  2  US-08-733-446-3           Sequence 3, Appli
   17     209    82.6     81  2  US-08-733-446-4           Sequence 4, Appli
   18     209    82.6     84  2  US-08-733-446-5           Sequence 5, Appli
   19     199    78.7     84  1  US-07-773-098-1           Sequence 1, Appli
   20     199    78.7     84  1  US-07-773-098-2           Sequence 2, Appli
   21     199    78.7     84  1  US-07-773-098-7           Sequence 7, Appli
   22     199    78.7     84  1  US-07-773-098-8           Sequence 8, Appli
   23     199    78.7     84  1  US-07-773-098-9           Sequence 9, Appli
   24     199    78.7     84  1  US-07-773-098-10          Sequence 10, Appl
   25     194    76.7     84  1  US-07-776-272-14          Sequence 14, Appl
   26      58    22.9   1120  4  US-09-147-404-1           Sequence 1, Appli
   27      55    21.7   1886  4  US-08-938-105-3           Sequence 3, Appli
   28    54.5    21.5    801  4  US-09-134-001C-5584       Sequence 5584, Ap
   29    52.5    20.8    185  4  US-09-154-083-14          Sequence 14, Appl
   30      52    20.6    133  4  US-08-961-083-188         Sequence 188, App
   31      52    20.6    287  1  US-08-624-125-17          Sequence 17, Appl
   32      51    20.2    706  1  US-08-339-152A-29         Sequence 29, Appl
   33      51    20.2    706  2  US-08-007-999B-4          Sequence 4, Appli
   34      51    20.2    706  2  US-08-689-276A-4          Sequence 4, Appli
   35      51    20.2    763  1  US-08-155-331-13          Sequence 13, Appl
   36      51    20.2    763  1  US-08-424-022-13          Sequence 13, Appl
   37      51    20.2    763  2  US-08-424-017B-13         Sequence 13, Appl
   38      51    20.2    763  5  PCT-US93-11696-13         Sequence 13, Appl
   39      51    20.2   2308  1  US-08-015-973-1           Sequence 1, Appli
   40      51    20.2   2308  2  US-08-448-164-1           Sequence 1, Appli
   41      51    20.2   2308  4  US-08-081-929-2           Sequence 2, Appli
   42      51    20.2   2314  4  US-09-816-703A-2          Sequence 2, Appli
   43      51    20.2  10182  4  US-09-134-001C-3159       Sequence 3159, Ap
   44    50.5    20.0    602  4  US-09-374-454-19          Sequence 19, Appl
   45      50    19.8    592  4  US-09-377-155-2           Sequence 2, Appli


                                 ALIGNMENTS


RESULT 1
US-09-044-536A-7
; Sequence 7, Application US/09044536A
; Patent No. 6025467
;  GENERAL INFORMATION:
;    APPLICANT:  FUKUDA, Tsunehiko
;    APPLICANT:  NAKAGAWA, Shizue
;    APPLICANT:  HABASHITA, Junko
;    APPLICANT:  TAKETOMI, Shigehisa
;    TITLE OF INVENTION:  PARATHYROID HORMONE DERIVATIVES AND THEIR USE
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DIKE, BRONSTEIN, ROBERTS & CUSHMAN
;      STREET:  130 Water Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  US
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/044,536A
;      FILING DATE:  19-MAR-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/662,871
;      FILING DATE:  12-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CONLIN, David G
;      REGISTRATION NUMBER:  27,026
;      REFERENCE/DOCKET NUMBER:  46509-DIV
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)523-3400
;      TELEFAX:  (617)523-6440
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  51 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  partial peptide
;      LOCATION:  1..51
US-09-044-536A-7

  Query Match             98.0%;  Score 248;  DB 3;  Length 51;
  Best Local Similarity   98.0%;  Pred. No. 5e-28;
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  Matches   50;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
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Db      1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEADKADVNVLTKAKSQ 51


RESULT 2
US-07-863-014-2
; Sequence 2, Application US/07863014
; Patent No. 5382658
;  GENERAL INFORMATION:
;    APPLICANT:  KRONIS, K. Anne
;    APPLICANT:  BOZZATO, Richard P.
;    TITLE OF INVENTION:  STABILITY-ENHANCED VARIANTS OF
;    TITLE OF INVENTION:  PARATHYROID HORMONE
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  1800 Diagonal Road, Suite 500
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  USA
;      ZIP:  22313-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/863,014
;      FILING DATE:  19920403
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  16777/163 ALLE
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)836-9300
;      TELEFAX:  (703)683-4109
;      TELEX:  899149
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  84 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-07-863-014-2

  Query Match             98.0%;  Score 248;  DB 1;  Length 84;
  Best Local Similarity   98.0%;  Pred. No. 9.5e-28;
  Matches   50;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
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Db     34 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEADKADVNVLTKAKSQ 84


RESULT 3
US-08-332-453-2
; Sequence 2, Application US/08332453
; Patent No. 5599792
;  GENERAL INFORMATION:
;    APPLICANT:  KRONIS, K. Anne
;    APPLICANT:  BOZZATO, Richard P.
;    TITLE OF INVENTION:  BONE-STIMULATING, NON-VASOACTIVE
;    TITLE OF INVENTION:  PARATHYROID HORMONE VARINATS
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  1800 Diagonal Road, Suite 500
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/332,453
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/900,680
;      FILING DATE:  19-JUN-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  16777/182 ALLE
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)836-9300
;      TELEFAX:  (703)683-4109
;      TELEX:  899149
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  84 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-332-453-2

  Query Match             98.0%;  Score 248;  DB 1;  Length 84;
  Best Local Similarity   98.0%;  Pred. No. 9.5e-28;
  Matches   50;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
          |||||||||||||||||||||||||||||||||||||:|||||||||||||
Db     34 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEADKADVNVLTKAKSQ 84


RESULT 4
US-08-689-190-2
; Sequence 2, Application US/08689190
; Patent No. 5714349
;  GENERAL INFORMATION:
;    APPLICANT:  FUKUDA, Tsunehiko
;    APPLICANT:  OSHIKA, Yuri
;    APPLICANT:  YAMADA, Takao
;    TITLE OF INVENTION:  SYNTHETIC GENE CODING FOR HUMAN
;    TITLE OF INVENTION:  PARATHYROID HORMONE
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
;      ADDRESSEE:  CUSHMAN
;      STREET:  130 Water Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  US
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/689,190
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/006,197
;      FILING DATE:
;      APPLICATION NUMBER:  US/08/016,171
;      FILING DATE:
;      APPLICATION NUMBER:  US/07/765,371
```

```
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WILLIAMS, Gregory D
;      REGISTRATION NUMBER:  30,901
;      REFERENCE/DOCKET NUMBER:  41,288
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)523-3400
;      TELEFAX:  (617)523-6440
;      TELEX:  200291 STRE UR
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  84 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-689-190-2

  Query Match             98.0%;  Score 248;  DB 1;  Length 84;
  Best Local Similarity   98.0%;  Pred. No. 9.5e-28;
  Matches   50;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
             |||||||||||||||||||||||||||||||||||||:|||||||||||||
Db      34 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEADKADVNVLTKAKSQ 84


RESULT 5
US-08-835-231-9
; Sequence 9, Application US/08835231
; Patent No. 5861284
;  GENERAL INFORMATION:
;    APPLICANT:  NISHIMURA, Osamu
;    APPLICANT:  KURIYAMA, Masato
;    APPLICANT:  KOYAMA, No. 5861284uyuki
;    APPLICANT:  FUKUDA, Tsunehiko
;    TITLE OF INVENTION:  METHOD FOR PRODUCING A BIOLOGICALLY
;    TITLE OF INVENTION:  ACTIVE RECOMBINANT CYSTEINE-FREE
;    NUMBER OF SEQUENCES:  37
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
;      STREET:  130 WATER STREET
;      CITY:  BOSTON
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/835,231
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/350,709
;      FILING DATE:  07-DEC-1994
;      APPLICATION NUMBER:  07/838,857
;      FILING DATE:  18-FEB-1992
;      APPLICATION NUMBER:  JP 024841
;      FILING DATE:  19-FEB-1991
;      APPLICATION NUMBER:  JP 0271438
;      FILING DATE:  18-OCT-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DAVID, RESNICK S
;      REGISTRATION NUMBER:  34,235
;      REFERENCE/DOCKET NUMBER:  41614-FWC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-523-3400
;      TELEFAX:  617-523-6440
;      TELEX:  200291 STRE
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  84 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
US-08-835-231-9

  Query Match             98.0%;  Score 248;  DB 2;  Length 84;
  Best Local Similarity   98.0%;  Pred. No. 9.5e-28;
  Matches   50;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
             |||||||||||||||||||||||||||||||||||||:|||||||||||||
Db      34 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEADKADVNVLTKAKSQ 84


RESULT 6
US-08-805-918-3
; Sequence 3, Application US/08805918
; Patent No. 5885821
;  GENERAL INFORMATION:
;    APPLICANT:  MAGOTA, Koji
;    APPLICANT:  MASUDA, Toyofumi
;    APPLICANT:  SUZUKI, Yuji
;    APPLICANT:  YABUTA, Masayuki
;    TITLE OF INVENTION:  PROCESS FOR PRODUCTION OF SECRETORY KEX2
;    TITLE OF INVENTION:  DERIVATIVES
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BURNS, DOANE, SWECKER & MATHIS
;      STREET:  P.O. Box 1404
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  United States
;      ZIP:  22313-1404
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/805,918
;      FILING DATE:  04-MAR-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 8-073217
;      FILING DATE:  04-MAR-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 8-352580
;      FILING DATE:  16-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meuth, Donna M.
;      REGISTRATION NUMBER:  36,607
;      REFERENCE/DOCKET NUMBER:  001560-295
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 836-6620
;      TELEFAX:  (703) 836-2021
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  84 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-805-918-3

  Query Match             98.0%;  Score 248;  DB 2;  Length 84;
  Best Local Similarity   98.0%;  Pred. No. 9.5e-28;
  Matches   50;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;
```

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Qy          1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
              |||||||||||||||||||||||||||||||||||||:|||||||||||||
Db         34 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEADKADVNVLTKAKSQ 84


RESULT 7
US-09-044-536A-36
; Sequence 36, Application US/09044536A
; Patent No. 6025467
;  GENERAL INFORMATION:
;    APPLICANT:  FUKUDA, Tsunehiko
;    APPLICANT:  NAKAGAWA, Shizue
;    APPLICANT:  HABASHITA, Junko
;    APPLICANT:  TAKETOMI, Shigehisa
;    TITLE OF INVENTION:  PARATHYROID HORMONE DERIVATIVES AND THEIR USE
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DIKE, BRONSTEIN, ROBERTS & CUSHMAN
;      STREET:  130 Water Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  US
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/044,536A
;      FILING DATE:  19-MAR-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/662,871
;      FILING DATE:  12-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CONLIN, David G
;      REGISTRATION NUMBER:  27,026
;      REFERENCE/DOCKET NUMBER:  46509-DIV
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)523-3400
;      TELEFAX:  (617)523-6440
;  INFORMATION FOR SEQ ID NO:  36:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  84 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  10
;      OTHER INFORMATION:  Xaa=acidic amino acid;
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  11
;      OTHER INFORMATION:  Xaa=hydrophobic alpha amino acid, basic
;      OTHER INFORMATION:  amino acid;
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  12
;      OTHER INFORMATION:  Xaa=Gly, Ala, Ser, Lys, Orn;
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  13
;      OTHER INFORMATION:  Xaa= basic amino acid;
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  14
;      OTHER INFORMATION:  Xaa= basic amino acid;
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  15
;      OTHER INFORMATION:  Xaa= aliphatic neutral amino acid, basic
;      OTHER INFORMATION:  amino acid;
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  16,17
;      OTHER INFORMATION:  Xaa= non-charged hydrophilic amino acid-
;      OTHER INFORMATION:  basic amino acid;
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  19
;      OTHER INFORMATION:  Xaa= acidic amino acid, basic amino acid;
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  21
;      OTHER INFORMATION:  Xaa= aliphatic neutral amino acid, basic
;      OTHER INFORMATION:  amino acid;
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  26
;      OTHER INFORMATION:  Xaa= basic amino acid;
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  27
;      OTHER INFORMATION:  Xaa= non-charged hydrophilic amino acid,
;      OTHER INFORMATION:  basic amino acid;
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  30
;      OTHER INFORMATION:  Xaa= acidic amino acid, aliphatic neutral
;      OTHER INFORMATION:  amino acid;
US-09-044-536A-36

  Query Match             98.0%;  Score 248;  DB 3;  Length 84;
  Best Local Similarity   98.0%;  Pred. No. 9.5e-28;
  Matches   50;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
              |||||||||||||||||||||||||||||||||||||:|||||||||||||
Db         34 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEADKADVNVLTKAKSQ 84


RESULT 8
US-09-108-661-9
; Sequence 9, Application US/09108661
; Patent No. 6287806
;  GENERAL INFORMATION:
;    APPLICANT:  NISHIMURA, Osamu
;    APPLICANT:  KURIYAMA, Masato
;    APPLICANT:  KOYAMA, No. 6287806uyuki
;    APPLICANT:  FUKUDA, Tsunehiko
;    TITLE OF INVENTION:  METHOD FOR PRODUCING A BIOLOGICALLY
;    TITLE OF INVENTION:  ACTIVE RECOMBINANT CYSTEINE-FREE
;    NUMBER OF SEQUENCES:  37
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
;      STREET:  130 WATER STREET
;      CITY:  BOSTON
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/108,661
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/350,709
;      FILING DATE:  07-DEC-1994
;      APPLICATION NUMBER:  07/838,857
;      FILING DATE:  18-FEB-1992
```

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;       APPLICATION NUMBER:  JP 024841
;       FILING DATE:  19-FEB-1991
;       APPLICATION NUMBER:  JP 0271438
;       FILING DATE:  18-OCT-1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  DAVID, RESNICK S
;       REGISTRATION NUMBER:  34,235
;       REFERENCE/DOCKET NUMBER:  41614-FWC
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  617-523-3400
;       TELEFAX:  617-523-6440
;       TELEX:  200291 STRE
;   INFORMATION FOR SEQ ID NO:  9:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  84 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
;     FRAGMENT TYPE:  N-terminal
;     ORIGINAL SOURCE:
US-09-108-661-9

  Query Match             98.0%;  Score 248;  DB 4;  Length 84;
  Best Local Similarity   98.0%;  Pred. No. 9.5e-28;
  Matches   50;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
             |||||||||||||||||||||||||||||||||||||:|||||||||||||
Db      34 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEADKADVNVLTKAKSQ 84


RESULT 9
PCT-US95-15800-25
; Sequence 25, Application PC/TUS9515800
;  GENERAL INFORMATION:
;    APPLICANT:  BioNebraska, Inc.
;    TITLE OF INVENTION:  PRODUCTION OF PEPTIDES USING
;    TITLE OF INVENTION:  RECOMBINANT FUSION PROTEIN CONSTRICTS
;    NUMBER OF SEQUENCES:  33
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Merchant & Gould
;      STREET:  3100 Norwest Center, 90 S. 7th Street
;      CITY:  Minneapolis
;      STATE:  MN
;      COUNTRY:  U.S.A.
;      ZIP:  55402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/15800
;      FILING DATE:  07-DEC-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/350,530
;      FILING DATE:  07-DEC-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Carter, Charles G
;      REGISTRATION NUMBER:  35,093
;      REFERENCE/DOCKET NUMBER:  8648.45USWO
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612/332-5300
;      TELEFAX:  612/332-9081
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  25:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  84 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  internal
;    ORIGINAL SOURCE:
PCT-US95-15800-25

  Query Match             98.0%;  Score 248;  DB 5;  Length 84;
  Best Local Similarity   98.0%;  Pred. No. 9.5e-28;
  Matches   50;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
             |||||||||||||||||||||||||||||||||||||:|||||||||||||
Db      34 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEADKADVNVLTKAKSQ 84


RESULT 10
US-08-142-551B-1
; Sequence 1, Application US/08142551B
; Patent No. 5814603
;  GENERAL INFORMATION:
;    APPLICANT:  Oldenburg, Kevin R.
;    APPLICANT:  Selick, Harold E.
;    TITLE OF INVENTION:  COMPOUNDS WITH PTH ACTIVITY AND
;    TITLE OF INVENTION:  RECOMBINANT DNA VECTORS ENCODING SAME
;    NUMBER OF SEQUENCES:  132
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Burns, Doane, Swecker & Mathis
;      STREET:  699 Prince Street
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  US
;      ZIP:  22313
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/142,551B
;      FILING DATE:  25-OCT-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/077,296
;      FILING DATE:  14-JUN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/898,219
;      FILING DATE:  12-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/965,677
;      FILING DATE:  22-OCT-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Swiss, Gerald F.
;      REGISTRATION NUMBER:  30,113
;      REFERENCE/DOCKET NUMBER:  000324-010
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 854-7400
;      TELEFAX:  (415) 854-8275
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  84 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  Protein
;      LOCATION:  1..84
;      OTHER INFORMATION:  /note= "84 amino acid PTH"
US-08-142-551B-1

  Query Match             96.0%;  Score 243;  DB 2;  Length 84;
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  Best Local Similarity   96.1%;  Pred. No. 4.8e-27;
  Matches   49;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
          |||||||||||||||||||||||||||||||||||||:||||:||||||||
Db     34 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEADKADVDVLTKAKSQ 84


RESULT 11
US-08-411-726-1
; Sequence 1, Application US/08411726
; Patent No. 5880093
;  GENERAL INFORMATION:
;    APPLICANT:  BAGNOLI, Franco
;    TITLE OF INVENTION:  Use of Parathormone, Its Biologically
;    TITLE OF INVENTION:  Active Fragments and Correlated Peptides, for The Preparation
;    TITLE OF INVENTION:  Pharmaceutical Compositions Useful for The Treatment of Pregna
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Kenyon & Kenyon
;      STREET:  1 Broadway
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  US
;      ZIP:  10004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS 6.2
;      SOFTWARE:  WordPerfect 6.1 for Windows
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/411,726
;      FILING DATE:  05-APR-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP93/02755
;      FILING DATE:  08-OCT-1993
;      APPLICATION NUMBER:  MI-92A002331
;      FILING DATE:  09-OCT-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  PALMESE, Maria Luisa
;      REGISTRATION NUMBER:  34,402
;      REFERENCE/DOCKET NUMBER:  2111/1300
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-425-7200
;      TELEFAX:  212-425-5288
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  84 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-411-726-1

  Query Match             96.0%;  Score 243;  DB 2;  Length 84;
  Best Local Similarity   96.1%;  Pred. No. 4.8e-27;
  Matches   49;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
          |||||||||||||||||||||||||||||||||||||:||||:||||||||
Db     34 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEADKADVDVLTKAKSQ 84


RESULT 12
US-07-707-114-1
; Sequence 1, Application US/07707114
; Patent No. 5208041
;  GENERAL INFORMATION:
;    APPLICANT:  SINDREY, Dennis R.
;    TITLE OF INVENTION:  ESSENTIALLY PURE HUMAN PARATHYROID
;    TITLE OF INVENTION:  HORMONE
;    NUMBER OF SEQUENCES:  1
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  1800 Diagonal Road, Suite 500
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/707,114
;      FILING DATE:  19910523
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  16777/147 ALLE
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)836-9300
;      TELEFAX:  (703)683-4109
;      TELEX:  899149
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  84 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    ORIGINAL SOURCE:
;      ORGANISM:  homo sapiens
;    IMMEDIATE SOURCE:
;      CLONE:  hPTH
US-07-707-114-1

  Query Match             94.1%;  Score 238;  DB 1;  Length 84;
  Best Local Similarity   94.1%;  Pred. No. 2.4e-26;
  Matches   48;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
          |||||||||||||||||||||||||||||||||||||:||:|:||||||||
Db     34 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEADKANVDVLTKAKSQ 84


RESULT 13
US-08-142-551B-119
; Sequence 119, Application US/08142551B
; Patent No. 5814603
;  GENERAL INFORMATION:
;    APPLICANT:  Oldenburg, Kevin R.
;    APPLICANT:  Selick, Harold E.
;    TITLE OF INVENTION:  COMPOUNDS WITH PTH ACTIVITY AND
;    TITLE OF INVENTION:  RECOMBINANT DNA VECTORS ENCODING SAME
;    NUMBER OF SEQUENCES:  132
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Burns, Doane, Swecker & Mathis
;      STREET:  699 Prince Street
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  US
;      ZIP:  22313
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/142,551B
;      FILING DATE:  25-OCT-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/077,296
```

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;       FILING DATE:  14-JUN-1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/898,219
;       FILING DATE:  12-JUN-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/965,677
;       FILING DATE:  22-OCT-1992
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Swiss, Gerald F.
;       REGISTRATION NUMBER:  30,113
;       REFERENCE/DOCKET NUMBER:  000324-010
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (415) 854-7400
;       TELEFAX:  (415) 854-8275
;   INFORMATION FOR SEQ ID NO:  119:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  50 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  unknown
;     MOLECULE TYPE:  protein
;     FEATURE:
;       NAME/KEY:  Protein
;       LOCATION:  1..50
;       OTHER INFORMATION:  /note= "Amino acid residues 34-84
;       OTHER INFORMATION:  of Human PTH."
US-08-142-551B-119

  Query Match             93.7%;  Score 237;  DB 2;  Length 50;
  Best Local Similarity   96.0%;  Pred. No. 1.7e-26;
  Matches   48;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        2 VALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
              ||||||||||||||||||||||||||||||||||||:||||:||||||||
Db        1 VALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEADKADVDVLTKAKSQ 50


RESULT 14
US-08-733-446-1
; Sequence 1, Application US/08733446
; Patent No. 5856138
;  GENERAL INFORMATION:
;     APPLICANT:  FUKUDA, Tsunehiko
;     TITLE OF INVENTION:  HUMAN PARATHYROID HORMONE MUTEINS AND
;     TITLE OF INVENTION:  PRODUCTION THEREOF
;     NUMBER OF SEQUENCES:  62
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
;       ADDRESSEE:  CUSHMAN
;       STREET:  130 Water Street
;       CITY:  Boston
;       STATE:  Massachusetts
;       COUNTRY:  US
;       ZIP:  02109
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/733,446
;       FILING DATE:  18-OCT-1996
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/402,970
;       FILING DATE:
;       APPLICATION NUMBER:  US/07/926,787
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  NEUNER, George W
;       REGISTRATION NUMBER:  26964
;       REFERENCE/DOCKET NUMBER:  42025
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (617)523-3400
```

```
;       TELEFAX:  (617)523-6440
;       TELEX:  200291 STRE UR
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  78 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
;     FEATURE:
;       NAME/KEY:  mutation
;       LOCATION:  2 Xaa=Leu, Ile, Val, Phe, Tyr, Trp or Met,
;       LOCATION:  12 Xaa=Leu, Ile, Val, Phe, Tyr, Trp or Met,
;       LOCATION:  28 Xaa=Cys or Phe,  29 Xaa=Cys or Val,
;       LOCATION:  31 Xaa=Cys or Leu,  33 Xaa=Cys or Ala,
;       LOCATION:  35 Xaa=Cys or Leu,  37 Xaa=Cys or Pro, 38 Xaa=Cys or Arg
;       IDENTIFICATION METHOD:  E
US-08-733-446-1

  Query Match             82.6%;  Score 209;  DB 2;  Length 78;
  Best Local Similarity   87.8%;  Pred. No. 2.7e-22;
  Matches   43;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        3 ALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
              | | | |  ||||||||||||||||||||||||||:|||||||||||||
Db       30 AXGXPXAXXDAGSQRPRKKEDNVLVESHEKSLGEADKADVNVLTKAKSQ 78


RESULT 15
US-08-733-446-2
; Sequence 2, Application US/08733446
; Patent No. 5856138
;  GENERAL INFORMATION:
;     APPLICANT:  FUKUDA, Tsunehiko
;     TITLE OF INVENTION:  HUMAN PARATHYROID HORMONE MUTEINS AND
;     TITLE OF INVENTION:  PRODUCTION THEREOF
;     NUMBER OF SEQUENCES:  62
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
;       ADDRESSEE:  CUSHMAN
;       STREET:  130 Water Street
;       CITY:  Boston
;       STATE:  Massachusetts
;       COUNTRY:  US
;       ZIP:  02109
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/733,446
;       FILING DATE:  18-OCT-1996
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/402,970
;       FILING DATE:
;       APPLICATION NUMBER:  US/07/926,787
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  NEUNER, George W
;       REGISTRATION NUMBER:  26964
;       REFERENCE/DOCKET NUMBER:  42025
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (617)523-3400
;       TELEFAX:  (617)523-6440
;       TELEX:  200291 STRE UR
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  79 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
;     FEATURE:
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;       NAME/KEY:  mutation
;       LOCATION:  3 Xaa=Leu, Ile, Val, Phe, Tyr, Trp or Met,
;       LOCATION:  13 Xaa=Leu, Ile, Val, Phe, Tyr, Trp or Met,
;       LOCATION:  29 Xaa=Cys or Phe,  30 Xaa=Cys or Val,
;       LOCATION:  32 Xaa=Cys or Leu,  34 Xaa=Cys or Ala,
;       LOCATION:  36 Xaa=Cys or Leu,  38 Xaa=Cys or Pro, 39 Xaa=Cys or Arg
;       IDENTIFICATION METHOD:  E
US-08-733-446-2

  Query Match             82.6%;  Score 209;  DB 2;  Length 79;
  Best Local Similarity   87.8%;  Pred. No. 2.7e-22;
  Matches   43;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       3 ALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
           | | | |  |||||||||||||||||||||||||:|||||||||||||
Db      31 AXGXPXAXXDAGSQRPRKKEDNVLVESHEKSLGEADKADVNVLTKAKSQ 79


Search completed: March 13, 2003, 14:52:54
Job time : 8.75373 secs
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                  GenCore version 5.1.4_p5_4578
         Copyright (c) 1993 - 2003  Compugen Ltd.


OM protein - protein search, using sw model

Run on:         March 13, 2003, 14:52:29 ; Search time 24.3582 Seconds
                                           (without alignments)
                                           278.993 Million cell updates/sec

Title:          US-09-636-530-3
Perfect score:  253
Sequence:       1 FVALGAPLAPRDAGSQRPRK..........KSLGEANKADVNVLTKAKSQ 51

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters:      908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       A_Geneseq_101002:*
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                2:  /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
                3:  /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
                4:  /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
                5:  /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
                6:  /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
                7:  /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
                8:  /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
                9:  /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
                10:  /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
                11:  /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*
                12:  /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
                13:  /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
                14:  /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:*
                15:  /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:*
                16:  /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:*
                17:  /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:*
                18:  /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*
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                22:  /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
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    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

                              SUMMARIES
               %
Result        Query
  No.  Score  Match Length DB  ID                     Description
-----------------------------------------------------------------------
   1    253  100.0     51  21  AAB07466               Amino acid sequenc
   2    253  100.0     82  21  AAB07465               Amino acid sequenc
   3    253  100.0     84  21  AAB07464               Amino acid sequenc
   4    248   98.0     51  18  AAW08107               Human parathyroid
   5    248   98.0     55  12  AAR11732               PTH-(29-84).  Synt
   6    248   98.0     78  14  AAR30852               hPTH mutein lackin
   7    248   98.0     78  14  AAR30859               Leu8 hPTH (7-84) m
   8    248   98.0     78  23  AAE23725               Human parathyroid
   9    248   98.0     78  23  AAU73024               Parathyroid hormon
  10    248   98.0     79  14  AAR30853               hPTH mutein lackin
  11    248   98.0     80  14  AAR35232               hPTH mutein lackin
  12    248   98.0     81  14  AAR30854               hPTH mutein lackin
  13    248   98.0     84  13  AAR23790               Parathyroid hormon
  14    248   98.0     84  13  AAR25571               Human PTH encoded
  15    248   98.0     84  13  AAR28845               Oxidation resistan
  16    248   98.0     84  13  AAR28846               Oxidation resistan
  17    248   98.0     84  13  AAR28847               Oxidation resistan
  18    248   98.0     84  13  AAR28848               Oxidation resistan
  19    248   98.0     84  13  AAR29561               Oxidation resistan
  20    248   98.0     84  13  AAR29562               Oxidation resistan
  21    248   98.0     84  13  AAR29563               Oxidation resistan
  22    248   98.0     84  13  AAR29564               Oxidation resistan
  23    248   98.0     84  13  AAR29565               Oxidation resistan
  24    248   98.0     84  13  AAR29566               Oxidation resistan
  25    248   98.0     84  13  AAR29567               Oxidation resistan
  26    248   98.0     84  13  AAR29568               Oxidation resistan
  27    248   98.0     84  14  AAR30860               Leu8, 18 hPTH mute
  28    248   98.0     84  14  AAR30857               Leu18 hPTH mutein.
  29    248   98.0     84  14  AAR42067               Human parathyroid
  30    248   98.0     84  14  AAR42068               Stability-enhanced
  31    248   98.0     84  14  AAR42069               Stability-enhanced
  32    248   98.0     84  14  AAR42070               Stability-enhanced
  33    248   98.0     84  14  AAR42071               Stability-enhanced
  34    248   98.0     84  14  AAR42072               Stability-enhanced
  35    248   98.0     84  14  AAR42073               Stability-enhanced
  36    248   98.0     84  14  AAR42074               Stability-enhanced
  37    248   98.0     84  14  AAR42075               Stability-enhanced
  38    248   98.0     84  14  AAR42076               Stability-enhanced
  39    248   98.0     84  14  AAR42077               Stability-enhanced
  40    248   98.0     84  15  AAR49692               Sequence of varian
  41    248   98.0     84  15  AAR49693               Sequence of varian
  42    248   98.0     84  15  AAR49694               Sequence of varian
  43    248   98.0     84  15  AAR49695               Sequence of varian
  44    248   98.0     84  15  AAR49696               Sequence of varian
  45    248   98.0     84  17  AAW29420               Human parathyroid


                              ALIGNMENTS


RESULT 1
AAB07466
ID   AAB07466 standard; protein; 51 AA.
XX
AC   AAB07466;
XX
DT   20-OCT-2000  (first entry)
XX
DE   Amino acid sequence of human parathyroid hormone antagonist.
XX
KW   Human; parathyroid hormone; PTH; hyperparathyroidism; bone disease.
XX
OS   Homo sapiens.
XX
PN   WO200042437-A1.
XX
PD   20-JUL-2000.
XX
PF   13-JAN-2000; 2000WO-US00855.
XX
PR   14-JAN-1999;   99US-0231422.
PR   26-JUN-1999;   99US-0344639.
XX
PA   (SCAN-) SCANTIBODIES LAB INC.
XX
DR   WPI; 2000-476147/41.
XX
PT   Differentiating between normal parathyroid function and
PT   hyperparathyroidism comprises determining and comparing whole
PT   parathyroid hormone, parathyroid hormone inhibitory peptide fragment
PT   and/or total parathyroid hormone levels -
XX
PS   Disclosure; Page 43; 46pp; English.
```

```
XX
CC   The present sequence represents a fragment of human parathyroid
CC   hormone (PTH), comprising residues 34-84, which functions as a PTH
CC   antagonist. The specification describes a method for differentiating
CC   between a person having substantially normal parathyroid function
CC   and having hyperparathyroidism. The method comprises determining and
CC   comparing at least two of the following parameters: whole parathyroid
CC   hormone level, parathyroid hormone inhibitory peptide fragment level
CC   and total parathyroid hormone level. The method is used for monitoring
CC   (treatments of) parathyroid related bone disease and the effects of
CC   therapeutic treatment for hyperparathyroidism.
XX
SQ   Sequence   51 AA;

  Query Match             100.0%;  Score 253;  DB 21;  Length 51;
  Best Local Similarity   100.0%;  Pred. No. 8.1e-27;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51


RESULT 2
AAB07465
ID   AAB07465 standard; protein; 82 AA.
XX
AC   AAB07465;
XX
DT   20-OCT-2000  (first entry)
XX
DE   Amino acid sequence of human parathyroid hormone antagonist.
XX
KW   Human; parathyroid hormone; PTH; hyperparathyroidism; bone disease.
XX
OS   Homo sapiens.
XX
PN   WO200042437-A1.
XX
PD   20-JUL-2000.
XX
PF   13-JAN-2000; 2000WO-US00855.
XX
PR   14-JAN-1999;   99US-0231422.
PR   26-JUN-1999;   99US-0344639.
XX
PA   (SCAN-) SCANTIBODIES LAB INC.
XX
DR   WPI; 2000-476147/41.
XX
PT   Differentiating between normal parathyroid function and
PT   hyperparathyroidism comprises determining and comparing whole
PT   parathyroid hormone, parathyroid hormone inhibitory peptide fragment
PT   and/or total parathyroid hormone levels -
XX
PS   Disclosure; Page 42-43; 46pp; English.
XX
CC   The present sequence represents a fragment of human parathyroid
CC   hormone (PTH), comprising residues 3-84, which functions as a PTH
CC   antagonist. The specification describes a method for differentiating
CC   between a person having substantially normal parathyroid function
CC   and having hyperparathyroidism. The method comprises determining and
CC   comparing at least two of the following parameters: whole parathyroid
CC   hormone level, parathyroid hormone inhibitory peptide fragment level
CC   and total parathyroid hormone level. The method is used for monitoring
CC   (treatments of) parathyroid related bone disease and the effects of
CC   therapeutic treatment for hyperparathyroidism.
XX
SQ   Sequence   82 AA;

  Query Match             100.0%;  Score 253;  DB 21;  Length 82;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-26;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy        1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       32 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 82


RESULT 3
AAB07464
ID   AAB07464 standard; protein; 84 AA.
XX
AC   AAB07464;
XX
DT   20-OCT-2000  (first entry)
XX
DE   Amino acid sequence of human parathyroid hormone.
XX
KW   Human; parathyroid hormone; PTH; hyperparathyroidism; bone disease.
XX
OS   Homo sapiens.
XX
PN   WO200042437-A1.
XX
PD   20-JUL-2000.
XX
PF   13-JAN-2000; 2000WO-US00855.
XX
PR   14-JAN-1999;   99US-0231422.
PR   26-JUN-1999;   99US-0344639.
XX
PA   (SCAN-) SCANTIBODIES LAB INC.
XX
DR   WPI; 2000-476147/41.
XX
PT   Differentiating between normal parathyroid function and
PT   hyperparathyroidism comprises determining and comparing whole
PT   parathyroid hormone, parathyroid hormone inhibitory peptide fragment
PT   and/or total parathyroid hormone levels -
XX
PS   Disclosure; Fig 1; 46pp; English.
XX
CC   The present sequence represents a human parathyroid hormone (PTH).
CC   Fragments of PTH function as PTH antagonists. The specification
CC   describes a method for differentiating between a person having
CC   substantially normal parathyroid function and having hyperparathyroidism.
CC   The method comprises determining and comparing at least two of the
CC   following parameters: whole parathyroid hormone level, parathyroid
CC   hormone inhibitory peptide fragment level and total parathyroid hormone
CC   level. The method is used for monitoring (treatments of) parathyroid
CC   related bone disease and the effects of therapeutic treatment for
CC   hyperparathyroidism.
XX
SQ   Sequence   84 AA;

  Query Match             100.0%;  Score 253;  DB 21;  Length 84;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-26;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       34 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 84


RESULT 4
AAW08107
ID   AAW08107 standard; peptide; 51 AA.
XX
AC   AAW08107;
XX
DT   10-OCT-1997  (first entry)
XX
DE   Human parathyroid hormone residues 34-84.
XX
KW   Human; parathyroid hormone; PTH; cAMP-producing activity;
```

```
KW   bone formation; osteoporosis; hypoparathyroidism; hypertension;
KW   climacteric disturbance.
XX
OS   Synthetic.
XX
PN   EP748817-A2.
XX
PD   18-DEC-1996.
XX
PF   13-JUN-1996;   96EP-0109475.
XX
PR   15-JUN-1995;   95JP-0148652.
XX
PA   (TAKE ) TAKEDA CHEM IND LTD.
XX
PI   Fukuda T,  Habashita J,  Nakagawa S,  Taketomi S;
XX
DR   WPI; 1997-036114/04.
XX
PT   New parathyroid hormone derivs.  - useful in treatment of bone
PT   diseases, hypoparathyroidism and hypertension
XX
PS   Claim 3; Page 39; 42pp; English.
XX
CC   The sequences given in AAW08103-07 represent fragments of human para-
CC   thyroid hormone (PTH) which were used as Xaa34 in the generic sequence
CC   given in AAW08102.  Peptides based on the generic sequence are human PTH
CC   (1-34) derivative peptides. They have potent cAMP-producing activity and
CC   bone formation activity.  They may be used in treatment of bone
CC   diseases including osteoporosis, hypoparathyroidism, hypertension
CC   and climacteric disturbance.  The peptides are low in toxicity and
CC   are safe.
XX
SQ   Sequence   51 AA;

  Query Match             98.0%;  Score 248;  DB 18;  Length 51;
  Best Local Similarity   98.0%;  Pred. No. 3.8e-26;
  Matches   50;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
          |||||||||||||||||||||||||||||||||||||:|||||||||||||
Db      1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEADKADVNVLTKAKSQ 51


RESULT 5
AAR11732
ID   AAR11732 standard; Protein; 55 AA.
XX
AC   AAR11732;
XX
DT   03-JUL-1991  (first entry)
XX
DE   PTH-(29-84).
XX
KW   Parathyroid hormone; calcium; osteoporosis; bone.
XX
OS   Synthetic.
XX
PN   WO9105050-A.
XX
PD   18-APR-1991.
XX
PF   01-OCT-1990;   90WO-C000335.
XX
PR   29-SEP-1989;   89CA-2615001.
XX
PA   (CANA ) NAT RES COUNCIL CAN.
XX
PI   Sung WL;
XX
DR   WPI; 1991-132857/18.
DR   N-PSDB; AAQ11618.
XX
PT   Mature human parathyroid synthesis - includes using eg E. coli
PT   transformed by plasmid contg. synthetic nucleotide sequence contg.
PT   adenine rich codons in N-terminal region.
XX
PS   Disclosure; Fig 6; 62pp; English.
XX
CC   Codons 29-84 are degenerate in the usage frequency favoured by
CC   E.coli or yeast. Codons 1-28 (see AAQ11617) are designed to contain
CC   adenine rich codons. The sequence is  prepd. from eight oligo-
CC   nucleotides (4 on each strand). A plasmid contg. the complete
CC   sequence expresses PTH with an improved yield. PTH is a blood
CC   calcium regulator known to increase bone mass.
XX
SQ   Sequence   55 AA;

  Query Match             98.0%;  Score 248;  DB 12;  Length 55;
  Best Local Similarity   98.0%;  Pred. No. 4.2e-26;
  Matches   50;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
          |||||||||||||||||||||||||||||||||||||:|||||||||||||
Db      5 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEADKADVNVLTKAKSQ 55


RESULT 6
AAR30852
ID   AAR30852 standard; Protein; 78 AA.
XX
AC   AAR30852;
XX
DT   09-JUN-1993  (first entry)
XX
DE   hPTH mutein lacking 6 N-terminal amino acids.
XX
KW   Human parathyroid hormone; hPTH; antagonist; hypoparathyroidism;
KW   hypercalcaemia.
XX
OS   Synthetic.
XX
PN   EP528271-A.
XX
PD   24-FEB-1993.
XX
PF   05-AUG-1992;   92EP-0113322.
XX
PR   07-AUG-1991;   91JP-0198056.
PR   26-JUN-1992;   92JP-0169713.
XX
PA   (TAKE ) TAKEDA CHEM IND LTD.
XX
PI   Fukuda T;
XX
DR   WPI; 1993-060187/08.
DR   N-PSDB; AAQ35228.
XX
PT   New human parathyroid mutein(s) - useful for treating e.g.
PT   osteoporosis, hypoparathyroidism, hyperparathyroidism,
PT   hypercalcaemia, hypertension etc.
XX
PS   Disclosure; Page 7; 88pp; English.
XX
CC   The sequence is that of a human parathyroid hormone (hPTH) peptide
CC   lacking 6 hPTH N-terminal amino acids. The peptide can have higher
CC   stability, enhanced activity and improved absorption by tissues.
CC   It can act as a PTH antagonist and can be used as a therapeutic
CC   agent for hypercalcaemia and hyperparathyroidism.
XX
SQ   Sequence   78 AA;

  Query Match             98.0%;  Score 248;  DB 14;  Length 78;
  Best Local Similarity   98.0%;  Pred. No. 6.5e-26;
  Matches   50;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy      1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
          ||||||||||||||||||||||||||||||||||||||:||||||||||||
Db     28 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEADKADVNVLTKAKSQ 78

RESULT 7
AAR30859
ID   AAR30859 standard; Protein; 78 AA.
XX
AC   AAR30859;
XX
DT   09-JUN-1993  (first entry)
XX
DE   Leu8 hPTH (7-84) mutein.
XX
KW   Human parathyroid hormone; hPTH; antagonist; hypoparathyroidism;
KW   hypercalcaemia.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Region          2
FT                   /note= "Met -> Leu"
XX
PN   EP528271-A.
XX
PD   24-FEB-1993.
XX
PF   05-AUG-1992;   92EP-0113322.
XX
PR   07-AUG-1991;   91JP-0198056.
PR   26-JUN-1992;   92JP-0169713.
XX
PA   (TAKE ) TAKEDA CHEM IND LTD.
XX
PI   Fukuda T;
XX
DR   WPI; 1993-060187/08.
DR   N-PSDB; AAQ36836.
XX
PT   New human parathyroid mutein(s) - useful for treating e.g.
PT   osteoporosis, hypoparathyroidism, hyperparathyroidism,
PT   hypercalcaemia, hypertension etc.
XX
PS   Example; Page 22; 88pp; English.
XX
CC   The sequence is that of mutated human parathyroid hormone (hPTH)
CC   (7-84) where Met8 is substd. by Leu. It has higher stability, enhanced
CC   activity and improved absorption by tissues. It can act as a PTH
CC   antagonist and can be used as a therapeutic agent for hypercalcaemia
CC   and hyperparathyroidism.
XX
SQ   Sequence   78 AA;

  Query Match             98.0%;  Score 248;  DB 14;  Length 78;
  Best Local Similarity   98.0%;  Pred. No. 6.5e-26;
  Matches   50;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
          ||||||||||||||||||||||||||||||||||||||:||||||||||||
Db     28 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEADKADVNVLTKAKSQ 78


RESULT 8
AAE23725
ID   AAE23725 standard; peptide; 78 AA.
XX
AC   AAE23725;
XX
DT   10-SEP-2002  (first entry)
XX
DE   Human parathyroid hormone (hPTH) peptide (7-84).
XX
```

```
KW   Human parathyroid hormone; hPTH; PTH-related peptide; PTHrP; eczema;
KW   hyperproliferative skin disorder; psoriasis; ichthyosis; skin cancer;
KW   acne; actinic keratosis; alopecia; gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO200228420-A2.
XX
PD   11-APR-2002.
XX
PF   05-OCT-2001; 2001WO-US31082.
XX
PR   06-OCT-2000; 2000US-238134P.
XX
PA   (HOLI/) HOLICK M F.
XX
PI   Holick MF;
XX
DR   WPI; 2002-452304/48.
DR   N-PSDB; AAD37995.
XX
PT   Regulating mammalian skin or hair cell proliferation and
PT   differentiation by administering nucleic acids encoding peptides
PT   derived from N-terminal region of human parathyroid hormone (hPTH) or
PT   hPTH-related protein  -
XX
PS   Claim 35; Fig 15; 56pp; English.
XX
CC   The invention relates to a method for regulating proliferation or
CC   enhancing differentiation of mammalian skin or hair cell. The method
CC   involves administering nucleic acids encoding peptides derived from
CC   N-terminal region of human parathyroid hormone (hPTH) or hPTH-related
CC   peptide (PTHrP). The method is used for inhibiting hyperproliferative
CC   skin disorders such as psoriasis, ichthyosis, eczema, acne, actinic
CC   keratosis, skin cancer, for inhibiting hair growth or preventing hair
CC   regrowth. It is useful for stimulating cell growth, rejuvenating aged
CC   skin, preventing skin wrinkles, treating skin wrinkles, enhancing wound
CC   healing, stimulating hair growth, maintaining hair growth, treating or
CC   preventing female or male pattern baldness, for treating chemotherapy
CC   induced alopecia and also for stimulating epidermal cell growth or
CC   hair follicle cell growth. The method is also used in gene therapy.
CC   The present sequence is hPTH peptide.
XX
SQ   Sequence   78 AA;

  Query Match             98.0%;  Score 248;  DB 23;  Length 78;
  Best Local Similarity   98.0%;  Pred. No. 6.5e-26;
  Matches   50;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
          ||||||||||||||||||||||||||||||||||||||:||||||||||||
Db     28 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEADKADVNVLTKAKSQ 78


RESULT 9
AAU73024
ID   AAU73024 standard; Peptide; 78 AA.
XX
AC   AAU73024;
XX
DT   12-MAR-2002  (first entry)
XX
DE   Parathyroid hormone PTH/PTHrP modulating domain #6.
XX
KW   Human; parathyroid hormone; PTH; parathyroid hormone-related protein;
KW   PTHrP; bone resorption inhibitor; osteoprotegrin; OPG; OPG-L antibody;
KW   calcitonin; bisphosphonate; oestrogen; oestrogen receptor; tibolone;
KW   osteopenia; hyperthyroidism; hypercalcaemia; tumour metastasis; bone;
KW   breast cancer; prostate cancer; cachexia; anorexia; osteoporosis;
KW   Paget's disease; osteomyelitis; osteonecrosis; bone cell death;
KW   Gaucher's disease; sickle cell anaemia; systemic lupus erythematosus;
KW   rheumatoid arthritis; periodontal disease; alopecia; fracture repair;
KW   immunoglobulin G; IgG.
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XX
OS   Homo sapiens.
XX
PN   WO200181415-A2.
XX
PD   01-NOV-2001.
XX
PF   27-APR-2001; 2001WO-US13528.
XX
PR   27-APR-2000; 2000US-200053P.
PR   28-JUN-2000; 2000US-214860P.
PR   06-FEB-2001; 2001US-266673P.
PR   26-APR-2001; 2001US-0843221.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Kostenuik P,  Liu C,  Lacey DL;
XX
DR   WPI; 2002-066435/09.
XX
PT   Composition, useful for treating osteopenia, comprises parathyroid
PT   hormone and parathyroid hormone-related protein receptor modulators -
XX
PS   Disclosure; Page 26; 107pp; English.
XX
CC   The invention relates to a composition (I) comprising modulators of
CC   parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHrP)
CC   which comprise a PTH/PTHrP modulating domain and a vehicle. (I)
CC   comprising PTH agonist optionally with a bone resorption inhibitor, such
CC   as osteoprotegrin (OPG), OPG-L antibody, calcitonin, bisphosphonates,
CC   oestrogens, oestrogen receptor modulators and tibolone is useful for
CC   treating osteopenia. (I) is useful for therapeutic and prophylactic
CC   purposes. Antagonists of PTH receptor are useful in treating primary and
CC   secondary hyperthyroidism, hypercalcaemia, tumour metastases,
CC   particularly breast and prostate cancer, cachexia and anorexia,
CC   osteopenia, including various forms of osteoporosis, Paget's disease of
CC   bone, osteomyelitis, osteonecrosis or bone cell death, associated with
CC   traumatic injury or nontraumatic necrosis associated with Gaucher's
CC   disease, sickle cell anaemia, systemic lupus erythematosus, rheumatoid
CC   arthritis, periodontal disease and alopecia. PTH receptor agonists are
CC   useful as therapeutic agents in conditions including fracture repair
CC   (including healing of non-union fractures), osteopenia, including various
CC   forms of osteoporosis. AAU73018-AAU73181 represent parathyroid hormone
CC   and parathyroid hormone related protein (PTH/PTHrP) modulators and
CC   related amino acid sequences of the invention.
XX
SQ   Sequence   78 AA;

  Query Match             98.0%;  Score 248;  DB 23;  Length 78;
  Best Local Similarity   98.0%;  Pred. No. 6.5e-26;
  Matches   50;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
             |||||||||||||||||||||||||||||||||||||:|||||||||||||
Db      28 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEADKADVNVLTKAKSQ 78


RESULT 10
AAR30853
ID   AAR30853 standard; Protein; 79 AA.
XX
AC   AAR30853;
XX
DT   09-JUN-1993  (first entry)
XX
DE   hPTH mutein lacking 5 N-terminal amino acids.
XX
KW   Human parathyroid hormone; hPTH; antagonist; hypoparathyroidism;
KW   hypercalcaemia.
XX
OS   Synthetic.
XX
PN   EP528271-A.
XX
PD   24-FEB-1993.
XX
PF   05-AUG-1992;   92EP-0113322.
XX
PR   07-AUG-1991;   91JP-0198056.
PR   26-JUN-1992;   92JP-0169713.
XX
PA   (TAKE ) TAKEDA CHEM IND LTD.
XX
PI   Fukuda T;
XX
DR   WPI; 1993-060187/08.
DR   N-PSDB; AAQ35229.
XX
PT   New human parathyroid mutein(s) - useful for treating e.g.
PT   osteoporosis, hypoparathyroidism, hyperparathyroidism,
PT   hypercalcaemia, hypertension etc.
XX
PS   Disclosure; Page 7; 88pp; English.
XX
CC   The sequence is that of a human parathyroid hormone (hPTH) peptide
CC   lacking 5 hPTH N-terminal amino acids. The peptide can have higher
CC   stability, enhanced activity and improved absorption by tissues.
CC   It can act as a PTH antagonist and can be used as a therapeutic
CC   agent for hypercalcaemia and hyperparathyroidism.
XX
SQ   Sequence   79 AA;

  Query Match             98.0%;  Score 248;  DB 14;  Length 79;
  Best Local Similarity   98.0%;  Pred. No. 6.6e-26;
  Matches   50;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
             |||||||||||||||||||||||||||||||||||||:|||||||||||||
Db      29 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEADKADVNVLTKAKSQ 79


RESULT 11
AAR35232
ID   AAR35232 standard; Protein; 80 AA.
XX
AC   AAR35232;
XX
DT   09-JUN-1993  (first entry)
XX
DE   hPTH mutein lacking 4 N-terminal amino acids.
XX
KW   Human parathyroid hormone; hPTH; antagonist; hypoparathyroidism;
KW   hypercalcaemia.
XX
OS   Synthetic.
XX
PN   EP528271-A.
XX
PD   24-FEB-1993.
XX
PF   05-AUG-1992;   92EP-0113322.
XX
PR   07-AUG-1991;   91JP-0198056.
PR   26-JUN-1992;   92JP-0169713.
XX
PA   (TAKE ) TAKEDA CHEM IND LTD.
XX
PI   Fukuda T;
XX
DR   WPI; 1993-060187/08.
DR   N-PSDB; AAQ35230.
XX
PT   New human parathyroid mutein(s) - useful for treating e.g.
PT   osteoporosis, hypoparathyroidism, hyperparathyroidism,
PT   hypercalcaemia, hypertension etc.
XX
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PS   Disclosure; Page 7; 88pp; English.
XX
CC   The sequence is that of a human parathyroid hormone (hPTH) peptide
CC   lacking 4 hPTH N-terminal amino acids. The peptide can have higher
CC   stability, enhanced activity and improved absorption by tissues.
CC   It can act as a PTH antagonist and can be used as a therapeutic
CC   agent for hypercalcaemia and hyperparathyroidism.
XX
SQ   Sequence   80 AA;

  Query Match             98.0%;  Score 248;  DB 14;  Length 80;
  Best Local Similarity   98.0%;  Pred. No. 6.7e-26;
  Matches   50;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
             |||||||||||||||||||||||||||||||||||||:|||||||||||||
Db      30 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEADKADVNVLTKAKSQ 80


RESULT 12
AAR30854
ID   AAR30854 standard; Protein; 81 AA.
XX
AC   AAR30854;
XX
DT   09-JUN-1993  (first entry)
XX
DE   hPTH mutein lacking 3 N-terminal amino acids.
XX
KW   Human parathyroid hormone; hPTH; antagonist; hypoparathyroidism;
KW   hypercalcaemia.
XX
OS   Synthetic.
XX
PN   EP528271-A.
XX
PD   24-FEB-1993.
XX
PF   05-AUG-1992;   92EP-0113322.
XX
PR   07-AUG-1991;   91JP-0198056.
PR   26-JUN-1992;   92JP-0169713.
XX
PA   (TAKE ) TAKEDA CHEM IND LTD.
XX
PI   Fukuda T;
XX
DR   WPI; 1993-060187/08.
DR   N-PSDB; AAQ36829.
XX
PT   New human parathyroid mutein(s) - useful for treating e.g.
PT   osteoporosis, hypoparathyroidism, hyperparathyroidism,
PT   hypercalcaemia, hypertension etc.
XX
PS   Disclosure; Page 7; 88pp; English.
XX
CC   The sequence is that of a human parathyroid hormone (hPTH) peptide
CC   lacking 3 hPTH N-terminal amino acids. The peptide can have higher
CC   stability, enhanced activity and improved absorption by tissues.
CC   It can act as a PTH antagonist and can be used as a therapeutic
CC   agent for hypercalcaemia and hyperparathyroidism.
XX
SQ   Sequence   81 AA;

  Query Match             98.0%;  Score 248;  DB 14;  Length 81;
  Best Local Similarity   98.0%;  Pred. No. 6.8e-26;
  Matches   50;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
             |||||||||||||||||||||||||||||||||||||:|||||||||||||
Db      31 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEADKADVNVLTKAKSQ 81
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RESULT 13
AAR23790
ID   AAR23790 standard; Protein; 84 AA.
XX
AC   AAR23790;
XX
DT   03-NOV-1992  (first entry)
XX
DE   Parathyroid hormone gene product.
XX
KW   hPTH; hypoparathyroidism; osteoporosis.
XX
OS   Synthetic.
XX
PN   EP483509-A.
XX
PD   06-MAY-1992.
XX
PF   25-SEP-1991;   91EP-0116281.
XX
PR   28-SEP-1990;   90JP-0257491.
PR   20-MAR-1991;   91JP-0056434.
XX
PA   (TAKE ) TAKEDA CHEM IND LTD.
XX
PI   Fukuda T,  Oshika Y,  Yamada T;
XX
DR   WPI; 1992-152248/19.
DR   N-PSDB; AAQ24478.
XX
PT   Synthetic gene encoding human parathyroid hormone - formed by
PT   ligating oligo-nucleotide(s) and expressed at high yield in E
PT   coli
XX
PS   Disclosure; Page 21; 33pp; English.
XX
CC   The human parathyroid hormone (hPTH) sequence given is the product of
CC   a synthetic gene which corresponds to the amino acid sequence of hPTH.
CC   The DNA sequence was produced by enzymatically ligating
CC   oligodeoxynucleotides.  hPTH is an important regulator of calcium
CC   metabolism and has clinical applicns. to diseases such as
CC   hypoparathyroidism and osteoporosis.  This hPTH  can be used as a
CC   therapeutic agent or to study the biological role of hPTH in vivo.
XX
SQ   Sequence   84 AA;

  Query Match             98.0%;  Score 248;  DB 13;  Length 84;
  Best Local Similarity   98.0%;  Pred. No. 7.1e-26;
  Matches   50;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
             |||||||||||||||||||||||||||||||||||||:|||||||||||||
Db      34 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEADKADVNVLTKAKSQ 84


RESULT 14
AAR25571
ID   AAR25571 standard; Protein; 84 AA.
XX
AC   AAR25571;
XX
DT   13-JAN-1993  (first entry)
XX
DE   Human PTH encoded by pX.
XX
KW   Parathyroid; hormone; osteoporosis; psoriasis; oxidation;
KW   resistance.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 8
FT                   /note= "see CC"
```

```
FT   Misc-difference 18
FT                   /note= "see CC"
XX
PN   WO9211286-A.
XX
PD   09-JUL-1992.
XX
PF   18-DEC-1991;   91WO-CA00451.
XX
PR   21-DEC-1990;   90US-0630969.
PR   13-DEC-1991;   91US-0806271.
XX
PA   (ALLE-) ALLELIX BIOPHARMACEUTICALS INC.
PA   (GLAX ) GLAXO CANADA INC.
XX
PI   Bozatto RP,  Kronis KA;
XX
DR   WPI; 1992-250028/30.
DR   N-PSDB; AAQ26498.
XX
PT   New oxidn. resistant variants of parathyroid hormone - used for
PT   treating osteoporosis, psoriasis and cardiovascular disorders
XX
PS   Disclosure; Fig 1; 40pp; English.
XX
CC   Variants of PTH exhibiting PTH activity and reduced sensitivity
CC   to oxidation are obtained by replacing at least one Met residue in
CC   PTH (positions 8 and 18) with a genetically encoded amino acid,
CC   other than Met and Cys.
CC   The Met amino acids are indicated in the Features Table.
CC   The variant may be obtd. using recombinant technique, and may be
CC   used for treating osteoporosis, other bone-related disorders,
CC   psoriasis and cardiovascular disorders.
CC   Human PTH refers to the mature form of the hormone, which consists
CC   of 84 amino acids arranged in the sequence reported by Kimura et al,
CC   1983, Biochem. Biophys. Res. Comm., 114(2):493.
CC   Examples of variants are given in AAR28845-48 and AAR29561-69.
XX
SQ   Sequence   84 AA;

  Query Match             98.0%;  Score 248;  DB 13;  Length 84;
  Best Local Similarity   98.0%;  Pred. No. 7.1e-26;
  Matches   50;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
          |||||||||||||||||||||||||||||||||||||:|||||||||||||
Db     34 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEADKADVNVLTKAKSQ 84


RESULT 15
AAR28845
ID   AAR28845 standard; Protein; 84 AA.
XX
AC   AAR28845;
XX
DT   13-JAN-1993  (first entry)
XX
DE   Oxidation resistant PTH variant (1).
XX
KW   Parathyroid; hormone; osteoporosis; psoriasis; oxidation;
KW   resistance.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 8
FT                   /label= ALA, VAL, LEU, ILE, SER, TRP
FT                   /note= "pref. Val, Leu or Ile"
XX
PN   WO9211286-A.
XX
PD   09-JUL-1992.
XX
PF   18-DEC-1991;   91WO-CA00451.
XX
PR   21-DEC-1990;   90US-0630969.
PR   13-DEC-1991;   91US-0806271.
XX
PA   (ALLE-) ALLELIX BIOPHARMACEUTICALS INC.
PA   (GLAX ) GLAXO CANADA INC.
XX
PI   Bozatto RP,  Kronis KA;
XX
DR   WPI; 1992-250028/30.
XX
PT   New oxidn. resistant variants of parathyroid hormone - used for
PT   treating osteoporosis, psoriasis and cardiovascular disorders
XX
PS   Claim 2-4; Page 30; 40pp; English.
XX
CC   Variants of PTH exhibiting PTH activity and reduced sensitivity
CC   to oxidation are obtained by replacing at least one Met residue in
CC   PTH (positions 8 and 18) with a genetically encoded amino acid,
CC   other than Met and Cys (see AAQ26498).
CC   The variant may be obtd. using recombinant technique, and may be
CC   used for treating osteoporosis, other bone-related disorders,
CC   psoriasis and cardiovascular disorders.
CC   Examples of variants are given in AAR28845-48 and AAR29561-69.
XX
SQ   Sequence   84 AA;

  Query Match             98.0%;  Score 248;  DB 13;  Length 84;
  Best Local Similarity   98.0%;  Pred. No. 7.1e-26;
  Matches   50;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
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Db     34 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEADKADVNVLTKAKSQ 84

Search completed: March 13, 2003, 15:00:26
Job time : 25.3582 secs
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                   GenCore version 5.1.4_p5_4578
          Copyright (c) 1993 - 2003  Compugen Ltd.


OM protein - protein search, using sw model

Run on:          March 13, 2003, 14:51:54 ; Search time 13.6269 Seconds
                                            (without alignments)
                                            280.743 Million cell updates/sec

Title:           US-09-636-530-2
Perfect score:   422
Sequence:        1 VSEIQLMHNLGKHLNSMERV..........KSLGEANKADVNVLTKAKSQ 83

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        199416 seqs, 46092074 residues

Total number of hits satisfying chosen parameters:      199416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Database :        Published_Applications_AA:*
                 1:  /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
                 2:  /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

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Result               Query
  No.    Score    Match Length DB  ID                          Description
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    1      422    100.0     83  9  US-09-928-047B-1             Sequence 1, Appli
    2      422    100.0     84  9  US-09-928-047B-5             Sequence 5, Appli
    3      418     99.1     82  9  US-09-928-047B-2             Sequence 2, Appli
    4      417     98.8     84  9  US-09-843-221A-10            Sequence 10, Appl
    5      417     98.8     84 10   US-09-169-786-1              Sequence 1, Appli
    6      400     94.8     78  9  US-09-928-047B-4             Sequence 4, Appli
    7      395     93.6     78  9  US-09-843-221A-12            Sequence 12, Appl
    8      359     85.1     84 10   US-09-879-257A-49            Sequence 49, Appl
    9      315     74.6     84  9  US-09-843-221A-11            Sequence 11, Appl
   10      286     67.8     57  9  US-09-928-047B-8             Sequence 8, Appli
   11      253     60.0     51  9  US-09-928-047B-3             Sequence 3, Appli
   12      247     58.5     50  9  US-09-928-047B-7             Sequence 7, Appli
   13      224     53.1     44  9  US-09-843-221A-13            Sequence 13, Appl
   14      193     45.7     37  9  US-09-843-221A-15            Sequence 15, Appl
   15      193     45.7     38  9  US-09-843-221A-14            Sequence 14, Appl
   16      193     45.7     38 10   US-09-169-786-4              Sequence 4, Appli
   17      188     44.5     40  9  US-10-014-162-111            Sequence 111, App
   18      175     41.5     34  9  US-09-928-047B-6             Sequence 6, Appli
   19      175     41.5     34  9  US-09-843-221A-16            Sequence 16, Appl
   20      175     41.5     34  9  US-09-843-221A-20            Sequence 20, Appl
   21      175     41.5     34  9  US-09-843-221A-161           Sequence 161, App
   22      175     41.5     34 10   US-09-169-786-3              Sequence 3, Appli
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   24      175     41.5     34 12   US-10-097-079-1              Sequence 1, Appli
   25      175     41.5     42  9  US-10-024-918-28             Sequence 28, Appl
   26      170     40.3     34  9  US-09-843-221A-19            Sequence 19, Appl
   27      170     40.3     34  9  US-09-843-221A-164           Sequence 164, App
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   29      170     40.3     34 12   US-10-016-403-7              Sequence 7, Appli
   30      169     40.0     34  9  US-09-843-221A-17            Sequence 17, Appl
   31      169     40.0     34  9  US-09-843-221A-18            Sequence 18, Appl
   32      169     40.0     34  9  US-09-843-221A-162           Sequence 162, App
   33      169     40.0     34  9  US-09-843-221A-163           Sequence 163, App
   34      167     39.6     34  9  US-09-843-221A-24            Sequence 24, Appl
   35      166     39.3     34  9  US-09-843-221A-21            Sequence 21, Appl
   36      166     39.3     34  9  US-09-843-221A-22            Sequence 22, Appl
   37      162     38.4     32  9  US-09-843-221A-29            Sequence 29, Appl
   38      162     38.4     32  9  US-09-843-221A-30            Sequence 30, Appl
   39      157     37.2     34  9  US-09-843-221A-23            Sequence 23, Appl
   40      157     37.2     34  9  US-09-843-221A-25            Sequence 25, Appl
   41      155     36.7     31  9  US-09-843-221A-27            Sequence 27, Appl
   42      155     36.7     31  9  US-09-843-221A-165           Sequence 165, App
   43      155     36.7     31 10   US-09-169-786-2              Sequence 2, Appli
   44      153     36.3     28  9  US-09-843-221A-32            Sequence 32, Appl
   45      153     36.3     32  9  US-09-843-221A-31            Sequence 31, Appl


                                  ALIGNMENTS


RESULT 1
US-09-928-047B-1
; Sequence 1, Application US/09928047B
; Patent No. US20020160945A1
; GENERAL INFORMATION:
;  APPLICANT: Cantor, Thomas
;  TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
;  TITLE OF INVENTION:  ANTAGONIST OR MODULATORS AND OSTEOPOROSIS
;  FILE REFERENCE: 53221-20002.00
;  CURRENT APPLICATION NUMBER: US/09/928,047B
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: US 60/224,446
;  PRIOR FILING DATE: 2000-08-10
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 83
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-928-047B-1

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Qy          1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
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Db          1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60

Qy         61 SHEKSLGEANKADVNVLTKAKSQ 83
              |||||||||||||||||||||||
Db         61 SHEKSLGEANKADVNVLTKAKSQ 83


RESULT 2
US-09-928-047B-5
; Sequence 5, Application US/09928047B
; Patent No. US20020160945A1
; GENERAL INFORMATION:
;  APPLICANT: Cantor, Thomas
;  TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
;  TITLE OF INVENTION:  ANTAGONIST OR MODULATORS AND OSTEOPOROSIS
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;  FILE REFERENCE: 53221-20002.00
;  CURRENT APPLICATION NUMBER: US/09/928,047B
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: US 60/224,446
;  PRIOR FILING DATE: 2000-08-10
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 84
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-928-047B-5

  Query Match             100.0%;  Score 422;  DB 9;  Length 84;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-42;
  Matches   83;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 61

Qy      61 SHEKSLGEANKADVNVLTKAKSQ 83
           |||||||||||||||||||||||
Db      62 SHEKSLGEANKADVNVLTKAKSQ 84

RESULT 3
US-09-928-047B-2
; Sequence 2, Application US/09928047B
; Patent No. US20020160945A1
; GENERAL INFORMATION:
;  APPLICANT: Cantor, Thomas
;  TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
;  TITLE OF INVENTION:  ANTAGONIST OR MODULATORS AND OSTEOPOROSIS
;  FILE REFERENCE: 53221-20002.00
;  CURRENT APPLICATION NUMBER: US/09/928,047B
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: US 60/224,446
;  PRIOR FILING DATE: 2000-08-10
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 82
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-928-047B-2

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Qy       2 SEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVES 61
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Qy      62 HEKSLGEANKADVNVLTKAKSQ 83
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Db      61 HEKSLGEANKADVNVLTKAKSQ 82

RESULT 4
US-09-843-221A-10
; Sequence 10, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTENUIK, PAUL
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  LACEY, DAVID LEE
;  TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
;  TITLE OF INVENTION:  RELATED PROTEIN
;  FILE REFERENCE: A-665B
;  CURRENT APPLICATION NUMBER: US/09/843,221A
;  CURRENT FILING DATE:  2001-04-26
;  PRIOR APPLICATION NUMBER: 60/266,673
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: 60/214,860
;  PRIOR FILING DATE: 2000-06-28
;  PRIOR APPLICATION NUMBER: 60/200,053
;  PRIOR FILING DATE: 2000-04-27
;  NUMBER OF SEQ ID NOS: 170
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
;   LENGTH: 84
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-843-221A-10

  Query Match             98.8%;  Score 417;  DB 9;  Length 84;
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Qy       1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 61

Qy      61 SHEKSLGEANKADVNVLTKAKSQ 83
           |||||||||:|||||||||||||
Db      62 SHEKSLGEADKADVNVLTKAKSQ 84

RESULT 5
US-09-169-786-1
; Sequence 1, Application US/09169786B
; Patent No. US20020025929A1
; GENERAL INFORMATION:
;  APPLICANT: Sato, Masahiko
;  TITLE OF INVENTION: METHOD OF BUILDING AND MAINTAINING BONE
;  FILE REFERENCE: X-11480
;  CURRENT APPLICATION NUMBER: US/09/169,786B
;  CURRENT FILING DATE: 1998-10-09
;  EARLIER APPLICATION NUMBER: US 60/061,800
;  EARLIER FILING DATE: 1997-10-14
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 84
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-169-786-1

  Query Match             98.8%;  Score 417;  DB 10;  Length 84;
  Best Local Similarity   98.8%;  Pred. No. 4.3e-42;
  Matches   82;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      61 SHEKSLGEANKADVNVLTKAKSQ 83
           |||||||||:|||||||||||||
Db      62 SHEKSLGEADKADVNVLTKAKSQ 84

RESULT 6
US-09-928-047B-4
; Sequence 4, Application US/09928047B
; Patent No. US20020160945A1
; GENERAL INFORMATION:
;  APPLICANT: Cantor, Thomas
;  TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
;  TITLE OF INVENTION:  ANTAGONIST OR MODULATORS AND OSTEOPOROSIS
;  FILE REFERENCE: 53221-20002.00
;  CURRENT APPLICATION NUMBER: US/09/928,047B
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: US 60/224,446
;  PRIOR FILING DATE: 2000-08-10
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;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 78
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-928-047B-4

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Qy      6 LMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVESHEKS 65
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 LMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVESHEKS 60

Qy     66 LGEANKADVNVLTKAKSQ 83
          ||||||||||||||||||
Db     61 LGEANKADVNVLTKAKSQ 78


RESULT 7
US-09-843-221A-12
; Sequence 12, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTENUIK, PAUL
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  LACEY, DAVID LEE
;  TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
;  TITLE OF INVENTION:  RELATED PROTEIN
;  FILE REFERENCE: A-665B
;  CURRENT APPLICATION NUMBER: US/09/843,221A
;  CURRENT FILING DATE:  2001-04-26
;  PRIOR APPLICATION NUMBER: 60/266,673
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: 60/214,860
;  PRIOR FILING DATE: 2000-06-28
;  PRIOR APPLICATION NUMBER: 60/200,053
;  PRIOR FILING DATE: 2000-04-27
;  NUMBER OF SEQ ID NOS: 170
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
;   LENGTH: 78
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-843-221A-12

  Query Match             93.6%;  Score 395;  DB 9;  Length 78;
  Best Local Similarity   98.7%;  Pred. No. 1.5e-39;
  Matches   77;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      6 LMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVESHEKS 65
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Db      1 LMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVESHEKS 60

Qy     66 LGEANKADVNVLTKAKSQ 83
          ||||:|||||||||||||
Db     61 LGEADKADVNVLTKAKSQ 78


RESULT 8
US-09-879-257A-49
; Sequence 49, Application US/09879257A
; Patent No. US20020081690A1
; GENERAL INFORMATION:
;  APPLICANT: YAMAMOTO, SACHIKO
;  APPLICANT:  HANADA, TOSHIRO
;  APPLICANT:  SHIRO, MINORU
;  APPLICANT:  KOBATAKE, SHINZO
;  TITLE OF INVENTION: HYBRID ENZYMES AND USE THEREOF
;  FILE REFERENCE: 55986(70281)
;  CURRENT APPLICATION NUMBER: US/09/879,257A
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;  CURRENT FILING DATE:  2001-06-12
;  NUMBER OF SEQ ID NOS: 56
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
;   LENGTH: 84
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-879-257A-49

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Db      2 VSEIQFMHNLGKHLSSMERVEWLRKKLQDVHNFVALGASIAYRDGSSQRPRKKEDNVLVE 61

Qy     61 SHEKSLGEANKADVNVLTKAKSQ 83
          ||:||||||:||||:|| ||| |
Db     62 SHQKSLGEADKADVDVLIKAKPQ 84


RESULT 9
US-09-843-221A-11
; Sequence 11, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTENUIK, PAUL
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  LACEY, DAVID LEE
;  TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROI
;  TITLE OF INVENTION:  RELATED PROTEIN
;  FILE REFERENCE: A-665B
;  CURRENT APPLICATION NUMBER: US/09/843,221A
;  CURRENT FILING DATE:  2001-04-26
;  PRIOR APPLICATION NUMBER: 60/266,673
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: 60/214,860
;  PRIOR FILING DATE: 2000-06-28
;  PRIOR APPLICATION NUMBER: 60/200,053
;  PRIOR FILING DATE: 2000-04-27
;  NUMBER OF SEQ ID NOS: 170
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
;   LENGTH: 84
;   TYPE: PRT
;   ORGANISM: Rattus rattus
US-09-843-221A-11

  Query Match             74.6%;  Score 315;  DB 9;  Length 84;
  Best Local Similarity   73.5%;  Pred. No. 4.1e-30;
  Matches   61;  Conservative   10;  Mismatches   12;  Indels    0;  Gaps    0;

Qy      1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
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Qy     61 SHEKSLGEANKADVNVLTKAKSQ 83
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Db     62 GNSKSLGEGDKADVDVLVKAKSQ 84


RESULT 10
US-09-928-047B-8
; Sequence 8, Application US/09928047B
; Patent No. US20020160945A1
; GENERAL INFORMATION:
;  APPLICANT: Cantor, Thomas
;  TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
;  TITLE OF INVENTION:  ANTAGONIST OR MODULATORS AND OSTEOPOROSIS
;  FILE REFERENCE: 53221-20002.00
;  CURRENT APPLICATION NUMBER: US/09/928,047B
;  CURRENT FILING DATE:  2001-08-10
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;  PRIOR APPLICATION NUMBER: US 60/224,446
;  PRIOR FILING DATE: 2000-08-10
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 57
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-928-047B-8

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Qy     27 LQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 83
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Db      1 LQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 57


RESULT 11
US-09-928-047B-3
; Sequence 3, Application US/09928047B
; Patent No. US20020160945A1
; GENERAL INFORMATION:
;  APPLICANT: Cantor, Thomas
;  TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
;  TITLE OF INVENTION:  ANTAGONIST OR MODULATORS AND OSTEOPOROSIS
;  FILE REFERENCE: 53221-20002.00
;  CURRENT APPLICATION NUMBER: US/09/928,047B
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: US 60/224,446
;  PRIOR FILING DATE: 2000-08-10
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 51
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-928-047B-3

  Query Match             60.0%;  Score 253;  DB 9;  Length 51;
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  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     33 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 83
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51


RESULT 12
US-09-928-047B-7
; Sequence 7, Application US/09928047B
; Patent No. US20020160945A1
; GENERAL INFORMATION:
;  APPLICANT: Cantor, Thomas
;  TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
;  TITLE OF INVENTION:  ANTAGONIST OR MODULATORS AND OSTEOPOROSIS
;  FILE REFERENCE: 53221-20002.00
;  CURRENT APPLICATION NUMBER: US/09/928,047B
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: US 60/224,446
;  PRIOR FILING DATE: 2000-08-10
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 50
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-928-047B-7

  Query Match             58.5%;  Score 247;  DB 9;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-22;
  Matches   50;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy     34 VALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 83
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 VALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 50

RESULT 13
US-09-843-221A-13
; Sequence 13, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTENUIK, PAUL
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  LACEY, DAVID LEE
;  TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROI
;  TITLE OF INVENTION:  RELATED PROTEIN
;  FILE REFERENCE: A-665B
;  CURRENT APPLICATION NUMBER: US/09/843,221A
;  CURRENT FILING DATE:  2001-04-26
;  PRIOR APPLICATION NUMBER: 60/266,673
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: 60/214,860
;  PRIOR FILING DATE: 2000-06-28
;  PRIOR APPLICATION NUMBER: 60/200,053
;  PRIOR FILING DATE: 2000-04-27
;  NUMBER OF SEQ ID NOS: 170
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
;   LENGTH: 44
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-843-221A-13

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  Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPR 43
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Db      2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPR 44


RESULT 14
US-09-843-221A-15
; Sequence 15, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTENUIK, PAUL
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  LACEY, DAVID LEE
;  TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROI
;  TITLE OF INVENTION:  RELATED PROTEIN
;  FILE REFERENCE: A-665B
;  CURRENT APPLICATION NUMBER: US/09/843,221A
;  CURRENT FILING DATE:  2001-04-26
;  PRIOR APPLICATION NUMBER: 60/266,673
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: 60/214,860
;  PRIOR FILING DATE: 2000-06-28
;  PRIOR APPLICATION NUMBER: 60/200,053
;  PRIOR FILING DATE: 2000-04-27
;  NUMBER OF SEQ ID NOS: 170
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
;   LENGTH: 37
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-843-221A-15

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  Best Local Similarity   100.0%;  Pred. No. 3.3e-16;
  Matches   37;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALG 37
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Db          1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALG 37


RESULT 15
US-09-843-221A-14
; Sequence 14, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTENUIK, PAUL
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  LACEY, DAVID LEE
;  TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
;  TITLE OF INVENTION:  RELATED PROTEIN
;  FILE REFERENCE: A-665B
;  CURRENT APPLICATION NUMBER: US/09/843,221A
;  CURRENT FILING DATE:  2001-04-26
;  PRIOR APPLICATION NUMBER: 60/266,673
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: 60/214,860
;  PRIOR FILING DATE: 2000-06-28
;  PRIOR APPLICATION NUMBER: 60/200,053
;  PRIOR FILING DATE: 2000-04-27
;  NUMBER OF SEQ ID NOS: 170
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
;   LENGTH: 38
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-843-221A-14

  Query Match             45.7%;  Score 193;  DB 9;  Length 38;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-16;
  Matches   37;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALG 37
              |||||||||||||||||||||||||||||||||||||
Db          2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALG 38


Search completed: March 13, 2003, 14:59:13
Job time : 14.6269 secs
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                    GenCore version 5.1.4_p5_4578
           Copyright (c) 1993 - 2003  Compugen Ltd.

OM protein - protein search, using sw model

Run on:         March 13, 2003, 14:51:54 ; Search time 8.37313 Seconds
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Title:          US-09-636-530-3
Perfect score:  253
Sequence:       1 FVALGAPLAPRDAGSQRPRK..........KSLGEANKADVNVLTKAKSQ 51

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       199416 seqs, 46092074 residues

Total number of hits satisfying chosen parameters:      199416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Published_Applications_AA:*
                1:  /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
                2:  /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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                13:  /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
                14:  /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                              SUMMARIES
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Result          Query
  No.   Score   Match Length DB  ID                          Description
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    1     253   100.0     51  9  US-09-928-047B-3             Sequence 3, Appli
    2     253   100.0     57  9  US-09-928-047B-8             Sequence 8, Appli
    3     253   100.0     78  9  US-09-928-047B-4             Sequence 4, Appli
    4     253   100.0     82  9  US-09-928-047B-2             Sequence 2, Appli
    5     253   100.0     83  9  US-09-928-047B-1             Sequence 1, Appli
    6     253   100.0     84  9  US-09-928-047B-5             Sequence 5, Appli
    7     248    98.0     78  9  US-09-843-221A-12            Sequence 12, Appl
    8     248    98.0     84  9  US-09-843-221A-10            Sequence 10, Appl
    9     248    98.0     84 10  US-09-169-786-1              Sequence 1, Appli
   10     247    97.6     50  9  US-09-928-047B-7             Sequence 7, Appli
   11     199    78.7     84 10  US-09-879-257A-49            Sequence 49, Appl
   12     164    64.8     84  9  US-09-843-221A-11            Sequence 11, Appl
   13      61    24.1    557 10  US-09-815-242-12165          Sequence 12165, A
   14      61    24.1    563 10  US-09-815-242-5464           Sequence 5464, Ap
   15      59    23.3    557 10  US-09-815-242-12804          Sequence 12804, A
   16      57    22.5    238 10  US-09-323-998D-41            Sequence 41, Appl
   17    55.5    21.9     46 10  US-09-864-761-34138          Sequence 34138, A
   18      55    21.7     44  9  US-09-843-221A-13            Sequence 13, Appl
   19      55    21.7   1157 10  US-09-935-291A-12            Sequence 12, Appl
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   20      55    21.7   1518 10  US-09-801-368-152            Sequence 152, App
   21      54    21.3   1033  9  US-09-820-843A-75            Sequence 75, Appl
   22      52    20.6    133 10  US-09-765-272-188            Sequence 188, App
   23      52    20.6    287 10  US-09-323-998D-17            Sequence 17, Appl
   24      52    20.6    682 10  US-09-815-242-11214          Sequence 11214, A
   25    51.5    20.4    797 10  US-09-815-242-4882           Sequence 4882, Ap
   26    51.5    20.4    798 10  US-09-815-242-10764          Sequence 10764, A
   27      51    20.2    307 10  US-09-323-998D-45            Sequence 45, Appl
   28      51    20.2   2308 12  US-10-000-954-2              Sequence 2, Appli
   29    50.5    20.0    318  9  US-09-738-626-4032           Sequence 4032, Ap
   30    50.5    20.0    591 10  US-09-764-864-1139           Sequence 1139, Ap
   31    50.5    20.0    596 10  US-09-797-039-8              Sequence 8, Appli
   32    50.5    20.0    602  9  US-10-121-235-19             Sequence 19, Appl
   33    50.5    20.0    739  9  US-10-160-663-2              Sequence 2, Appli
   34    50.5    20.0   1051  9  US-09-976-059-13             Sequence 13, Appl
   35      50    19.8    592 10  US-09-797-862-2              Sequence 2, Appli
   36      50    19.8    913 10  US-09-848-294-2              Sequence 2, Appli
   37      50    19.8   1464  9  US-09-842-777-10             Sequence 10, Appl
   38    49.5    19.6    243  9  US-09-746-783-210            Sequence 210, App
   39    49.5    19.6    491  9  US-09-853-257-2              Sequence 2, Appli
   40    49.5    19.6    655  9  US-09-738-626-4563           Sequence 4563, Ap
   41    49.5    19.6   1616  9  US-09-820-843A-16            Sequence 16, Appl
   42      49    19.4    141  9  US-09-764-868-1046           Sequence 1046, Ap
   43      49    19.4    172 10  US-09-734-017A-2             Sequence 2, Appli
   44      49    19.4    184 10  US-09-764-864-1280           Sequence 1280, Ap
   45      49    19.4    238  9  US-09-738-626-4368           Sequence 4368, Ap

                              ALIGNMENTS

RESULT 1
US-09-928-047B-3
; Sequence 3, Application US/09928047B
; Patent No. US20020160945A1
; GENERAL INFORMATION:
;  APPLICANT: Cantor, Thomas
;  TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
;  TITLE OF INVENTION:  ANTAGONIST OR MODULATORS AND OSTEOPOROSIS
;  FILE REFERENCE: 53221-20002.00
;  CURRENT APPLICATION NUMBER: US/09/928,047B
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: US 60/224,446
;  PRIOR FILING DATE: 2000-08-10
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 51
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-928-047B-3

  Query Match             100.0%;  Score 253;  DB 9;  Length 51;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-26;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51


RESULT 2
US-09-928-047B-8
; Sequence 8, Application US/09928047B
; Patent No. US20020160945A1
; GENERAL INFORMATION:
;  APPLICANT: Cantor, Thomas
;  TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
;  TITLE OF INVENTION:  ANTAGONIST OR MODULATORS AND OSTEOPOROSIS
;  FILE REFERENCE: 53221-20002.00
;  CURRENT APPLICATION NUMBER: US/09/928,047B
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: US 60/224,446
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;  PRIOR FILING DATE: 2000-08-10
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 57
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-928-047B-8

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  Best Local Similarity   100.0%;  Pred. No. 3.7e-26;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
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Db       7 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 57


RESULT 3
US-09-928-047B-4
; Sequence 4, Application US/09928047B
; Patent No. US20020160945A1
; GENERAL INFORMATION:
;  APPLICANT: Cantor, Thomas
;  TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
;  TITLE OF INVENTION:  ANTAGONIST OR MODULATORS AND OSTEOPOROSIS
;  FILE REFERENCE: 53221-20002.00
;  CURRENT APPLICATION NUMBER: US/09/928,047B
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: US 60/224,446
;  PRIOR FILING DATE: 2000-08-10
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 78
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-928-047B-4

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  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
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Db      28 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 78


RESULT 4
US-09-928-047B-2
; Sequence 2, Application US/09928047B
; Patent No. US20020160945A1
; GENERAL INFORMATION:
;  APPLICANT: Cantor, Thomas
;  TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
;  TITLE OF INVENTION:  ANTAGONIST OR MODULATORS AND OSTEOPOROSIS
;  FILE REFERENCE: 53221-20002.00
;  CURRENT APPLICATION NUMBER: US/09/928,047B
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: US 60/224,446
;  PRIOR FILING DATE: 2000-08-10
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 82
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-928-047B-2

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  Best Local Similarity   100.0%;  Pred. No. 5.8e-26;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy       1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
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Db      32 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 82


RESULT 5
US-09-928-047B-1
; Sequence 1, Application US/09928047B
; Patent No. US20020160945A1
; GENERAL INFORMATION:
;  APPLICANT: Cantor, Thomas
;  TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
;  TITLE OF INVENTION:  ANTAGONIST OR MODULATORS AND OSTEOPOROSIS
;  FILE REFERENCE: 53221-20002.00
;  CURRENT APPLICATION NUMBER: US/09/928,047B
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: US 60/224,446
;  PRIOR FILING DATE: 2000-08-10
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 83
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-928-047B-1

  Query Match             100.0%;  Score 253;  DB 9;  Length 83;
  Best Local Similarity   100.0%;  Pred. No. 5.9e-26;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      33 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 83


RESULT 6
US-09-928-047B-5
; Sequence 5, Application US/09928047B
; Patent No. US20020160945A1
; GENERAL INFORMATION:
;  APPLICANT: Cantor, Thomas
;  TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
;  TITLE OF INVENTION:  ANTAGONIST OR MODULATORS AND OSTEOPOROSIS
;  FILE REFERENCE: 53221-20002.00
;  CURRENT APPLICATION NUMBER: US/09/928,047B
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: US 60/224,446
;  PRIOR FILING DATE: 2000-08-10
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 84
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-928-047B-5

  Query Match             100.0%;  Score 253;  DB 9;  Length 84;
  Best Local Similarity   100.0%;  Pred. No. 6e-26;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
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Db      34 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 84


RESULT 7
US-09-843-221A-12
; Sequence 12, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTENUIK, PAUL
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  LACEY, DAVID LEE
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;  TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
;  TITLE OF INVENTION:  RELATED PROTEIN
;  FILE REFERENCE: A-665B
;  CURRENT APPLICATION NUMBER: US/09/843,221A
;  CURRENT FILING DATE:  2001-04-26
;  PRIOR APPLICATION NUMBER: 60/266,673
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: 60/214,860
;  PRIOR FILING DATE: 2000-06-28
;  PRIOR APPLICATION NUMBER: 60/200,053
;  PRIOR FILING DATE: 2000-04-27
;  NUMBER OF SEQ ID NOS: 170
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
;   LENGTH: 78
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-843-221A-12

  Query Match             98.0%;  Score 248;  DB 9;  Length 78;
  Best Local Similarity   98.0%;  Pred. No. 2.4e-25;
  Matches   50;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
           |||||||||||||||||||||||||||||||||||||:|||||||||||||
Db      28 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEADKADVNVLTKAKSQ 78


RESULT 8
US-09-843-221A-10
; Sequence 10, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTENUIK, PAUL
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  LACEY, DAVID LEE
;  TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
;  TITLE OF INVENTION:  RELATED PROTEIN
;  FILE REFERENCE: A-665B
;  CURRENT APPLICATION NUMBER: US/09/843,221A
;  CURRENT FILING DATE:  2001-04-26
;  PRIOR APPLICATION NUMBER: 60/266,673
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: 60/214,860
;  PRIOR FILING DATE: 2000-06-28
;  PRIOR APPLICATION NUMBER: 60/200,053
;  PRIOR FILING DATE: 2000-04-27
;  NUMBER OF SEQ ID NOS: 170
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
;   LENGTH: 84
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-843-221A-10

  Query Match             98.0%;  Score 248;  DB 9;  Length 84;
  Best Local Similarity   98.0%;  Pred. No. 2.7e-25;
  Matches   50;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
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Db      34 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEADKADVNVLTKAKSQ 84

RESULT 9
US-09-169-786-1
; Sequence 1, Application US/09169786B
; Patent No. US20020025929A1
; GENERAL INFORMATION:
;  APPLICANT: Sato, Masahiko
;  TITLE OF INVENTION: METHOD OF BUILDING AND MAINTAINING BONE
;  FILE REFERENCE: X-11480
;  CURRENT APPLICATION NUMBER: US/09/169,786B
;  CURRENT FILING DATE: 1998-10-09
;  EARLIER APPLICATION NUMBER: US 60/061,800
;  EARLIER FILING DATE: 1997-10-14
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 84
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-169-786-1

  Query Match             98.0%;  Score 248;  DB 10;  Length 84;
  Best Local Similarity   98.0%;  Pred. No. 2.7e-25;
  Matches   50;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
           |||||||||||||||||||||||||||||||||||||:|||||||||||||
Db      34 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEADKADVNVLTKAKSQ 84

RESULT 10
US-09-928-047B-7
; Sequence 7, Application US/09928047B
; Patent No. US20020160945A1
; GENERAL INFORMATION:
;  APPLICANT: Cantor, Thomas
;  TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
;  TITLE OF INVENTION:  ANTAGONIST OR MODULATORS AND OSTEOPOROSIS
;  FILE REFERENCE: 53221-20002.00
;  CURRENT APPLICATION NUMBER: US/09/928,047B
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: US 60/224,446
;  PRIOR FILING DATE: 2000-08-10
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 50
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-928-047B-7

  Query Match             97.6%;  Score 247;  DB 9;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-25;
  Matches   50;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 VALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 VALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 50

RESULT 11
US-09-879-257A-49
; Sequence 49, Application US/09879257A
; Patent No. US20020081690A1
; GENERAL INFORMATION:
;  APPLICANT: YAMAMOTO, SACHIKO
;  APPLICANT:  HANADA, TOSHIRO
;  APPLICANT:  SHIRO, MINORU
;  APPLICANT:  KOBATAKE, SHINZO
;  TITLE OF INVENTION: HYBRID ENZYMES AND USE THEREOF
;  FILE REFERENCE: 55986(70281)
;  CURRENT APPLICATION NUMBER: US/09/879,257A
;  CURRENT FILING DATE:  2001-06-12
;  NUMBER OF SEQ ID NOS: 56
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
;   LENGTH: 84
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-879-257A-49

  Query Match             78.7%;  Score 199;  DB 10;  Length 84;
  Best Local Similarity   80.4%;  Pred. No. 6.1e-19;
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  Matches   41;  Conservative    4;  Mismatches    6; . Indels    0;  Gaps    0;

Qy          1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
              |||||| :| ||  ||||||||||||||||:||||||:||||:|| ||| |
Db         34 FVALGASIAYRDGSSQRPRKKEDNVLVESHQKSLGEADKADVDVLIKAKPQ 84


RESULT 12
US-09-843-221A-11
; Sequence 11, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTENUIK, PAUL
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  LACEY, DAVID LEE
;  TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
;  TITLE OF INVENTION:  RELATED PROTEIN
;  FILE REFERENCE: A-665B
;  CURRENT APPLICATION NUMBER: US/09/843,221A
;  CURRENT FILING DATE:  2001-04-26
;  PRIOR APPLICATION NUMBER: 60/266,673
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: 60/214,860
;  PRIOR FILING DATE: 2000-06-28
;  PRIOR APPLICATION NUMBER: 60/200,053
;  PRIOR FILING DATE: 2000-04-27
;  NUMBER OF SEQ ID NOS: 170
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
;   LENGTH: 84
;   TYPE: PRT
;   ORGANISM: Rattus rattus
US-09-843-221A-11

  Query Match             64.8%;  Score 164;  DB 9;  Length 84;
  Best Local Similarity   64.7%;  Pred. No. 2.1e-14;
  Matches   33;  Conservative    7;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
              ||:||  :| |:   ||| ||||||||: : ||||| :||||:|| |||||
Db         34 FVSLGVQMAAREGSYQRPTKKEDNVLVDGNSKSLGEGDKADVDVLVKAKSQ 84


RESULT 13
US-09-815-242-12165
; Sequence 12165, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
;  APPLICANT: Haselbeck, Robert
;  APPLICANT:  Ohlsen, Kari L.
;  APPLICANT:  Zyskind, Judith W.
;  APPLICANT:  Wall, Daniel
;  APPLICANT:  Trawick, John D.
;  APPLICANT:  Carr, Grant J.
;  APPLICANT:  Yamamoto, Robert T.
;  APPLICANT:  Xu, H. Howard
;  TITLE OF INVENTION: Identification of Essential Genes in
;  TITLE OF INVENTION:  Prokaryotes
;  FILE REFERENCE: ELITRA.011A
;  CURRENT APPLICATION NUMBER: US/09/815,242
;  CURRENT FILING DATE:  2001-03-21
;  PRIOR APPLICATION NUMBER: 60/191,078
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: 60/206,848
;  PRIOR FILING DATE: 2000-05-23
;  PRIOR APPLICATION NUMBER: 60/207,727
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: 60/242,578
;  PRIOR FILING DATE: 2000-10-23
;  PRIOR APPLICATION NUMBER: 60/253,625
;  PRIOR FILING DATE: 2000-11-27
;  PRIOR APPLICATION NUMBER: 60/257,931
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: 60/269,308
;  PRIOR FILING DATE: 2001-02-16
;  NUMBER OF SEQ ID NOS: 14110
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12165
;   LENGTH: 557
;   TYPE: PRT
;   ORGANISM: Staphylococcus aureus
US-09-815-242-12165

  Query Match             24.1%;  Score 61;  DB 10;  Length 557;
  Best Local Similarity   31.9%;  Pred. No. 5.3;
  Matches   15;  Conservative   11;  Mismatches   17;  Indels    4;  Gaps    1;

Qy          3 ALGAPLAPRDAGSQRP----RKKEDNVLVESHEKSLGEANKADVNVL 45
              | |  :||    |::|    :| ::   ::   | | :|||||: :|
Db        383 AQGVSVAPTQKSSKKPARGIQKSKNAFSMQQIAKVLDKANKADIKLL 429


RESULT 14
US-09-815-242-5464
; Sequence 5464, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
;  APPLICANT: Haselbeck, Robert
;  APPLICANT:  Ohlsen, Kari L.
;  APPLICANT:  Zyskind, Judith W.
;  APPLICANT:  Wall, Daniel
;  APPLICANT:  Trawick, John D.
;  APPLICANT:  Carr, Grant J.
;  APPLICANT:  Yamamoto, Robert T.
;  APPLICANT:  Xu, H. Howard
;  TITLE OF INVENTION: Identification of Essential Genes in
;  TITLE OF INVENTION:  Prokaryotes
;  FILE REFERENCE: ELITRA.011A
;  CURRENT APPLICATION NUMBER: US/09/815,242
;  CURRENT FILING DATE:  2001-03-21
;  PRIOR APPLICATION NUMBER: 60/191,078
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: 60/206,848
;  PRIOR FILING DATE: 2000-05-23
;  PRIOR APPLICATION NUMBER: 60/207,727
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: 60/242,578
;  PRIOR FILING DATE: 2000-10-23
;  PRIOR APPLICATION NUMBER: 60/253,625
;  PRIOR FILING DATE: 2000-11-27
;  PRIOR APPLICATION NUMBER: 60/257,931
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: 60/269,308
;  PRIOR FILING DATE: 2001-02-16
;  NUMBER OF SEQ ID NOS: 14110
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5464
;   LENGTH: 563
;   TYPE: PRT
;   ORGANISM: Staphylococcus aureus
US-09-815-242-5464

  Query Match             24.1%;  Score 61;  DB 10;  Length 563;
  Best Local Similarity   31.9%;  Pred. No. 5.3;
  Matches   15;  Conservative   11;  Mismatches   17;  Indels    4;  Gaps    1;

Qy          3 ALGAPLAPRDAGSQRP----RKKEDNVLVESHEKSLGEANKADVNVL 45
              | |  :||    |::|    :| ::   ::   | | :|||||: :|
Db        391 AQGVSVAPTQKSSKKPARGIQKSKNAFSMQQIAKVLDKANKADIKLL 437


RESULT 15
US-09-815-242-12804
; Sequence 12804, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
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;  APPLICANT: Haselbeck, Robert
;  APPLICANT:  Ohlsen, Kari L.
;  APPLICANT:  Zyskind, Judith W.
;  APPLICANT:  Wall, Daniel
;  APPLICANT:  Trawick, John D.
;  APPLICANT:  Carr, Grant J.
;  APPLICANT:  Yamamoto, Robert T.
;  APPLICANT:  Xu, H. Howard
;  TITLE OF INVENTION: Identification of Essential Genes in
;  TITLE OF INVENTION:  Prokaryotes
;  FILE REFERENCE: ELITRA.011A
;  CURRENT APPLICATION NUMBER: US/09/815,242
;  CURRENT FILING DATE:  2001-03-21
;  PRIOR APPLICATION NUMBER: 60/191,078
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: 60/206,848
;  PRIOR FILING DATE: 2000-05-23
;  PRIOR APPLICATION NUMBER: 60/207,727
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: 60/242,578
;  PRIOR FILING DATE: 2000-10-23
;  PRIOR APPLICATION NUMBER: 60/253,625
;  PRIOR FILING DATE: 2000-11-27
;  PRIOR APPLICATION NUMBER: 60/257,931
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: 60/269,308
;  PRIOR FILING DATE: 2001-02-16
;  NUMBER OF SEQ ID NOS: 14110
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12804
;   LENGTH: 557
;   TYPE: PRT
;   ORGANISM: Staphylococcus aureus
US-09-815-242-12804

  Query Match             23.3%;  Score 59;  DB 10;  Length 557;
  Best Local Similarity   31.9%;  Pred. No. 9.6;
  Matches   15;  Conservative   11;  Mismatches   17;  Indels    4;  Gaps    1;

Qy        3 ALGAPLAPRDAGSQRP----RKKEDNVLVESHEKSLGEANKADVNVL 45
            | |  :||    |::|    :| ::   ::   | | :|||||: :|
Db      383 AQGVSVAPVQKSSKKPARGIQKSKNAFSMQQIAKVLDKANKADIKLL 429


Search completed: March 13, 2003, 14:59:14
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                  GenCore version 5.1.4_p5_4578
            Copyright (c) 1993 - 2003  Compugen Ltd.

OM protein - protein search, using sw model

Run on:         March 13, 2003, 14:48:44 ; Search time 108.47 Seconds
                                           (without alignments)
                                           303.138 Million cell updates/sec

Title:          US-09-636-530-3
Perfect score:  253
Sequence:       1 FVALGAPLAPRDAGSQRPRK..........KSLGEANKADVNVLTKAKSQ 51

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters:      4569144

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Pending_Patents_AA_Main:*
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                2:  /cgn2_6/ptodata/2/paa/US06_COMB.pep:*
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                6:  /cgn2_6/ptodata/2/paa/US082_COMB.pep:*
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                11:  /cgn2_6/ptodata/2/paa/US087_COMB.pep:*
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                13:  /cgn2_6/ptodata/2/paa/US089_COMB.pep:*
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                15:  /cgn2_6/ptodata/2/paa/US091_COMB.pep:*
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                19:  /cgn2_6/ptodata/2/paa/US095_COMB.pep:*
                20:  /cgn2_6/ptodata/2/paa/US096_COMB.pep:*
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                22:  /cgn2_6/ptodata/2/paa/US098_COMB.pep:*
                23:  /cgn2_6/ptodata/2/paa/US099_COMB.pep:*
                24:  /cgn2_6/ptodata/2/paa/US100_COMB.pep:*
                25:  /cgn2_6/ptodata/2/paa/US101_COMB.pep:*
                26:  /cgn2_6/ptodata/2/paa/US102_COMB.pep:*
                27:  /cgn2_6/ptodata/2/paa/US60_COMB.pep:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                 SUMMARIES
                       %
Result                Query
  No.     Score   Match  Length  DB  ID                          Description
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    1      253   100.0     51  17  US-09-323-606C-3            Sequence 3, Appli
    2      253   100.0     51  20  US-09-636-530-3             Sequence 3, Appli
    3      253   100.0     51  23  US-09-928-047B-3            Sequence 3, Appli
    4      253   100.0     51  23  US-09-928-048A-5            Sequence 5, Appli
    5      253   100.0     57  20  US-09-636-530-5             Sequence 5, Appli
    6      253   100.0     57  23  US-09-928-047B-8            Sequence 8, Appli
    7      253   100.0     67  17  US-09-323-606C-11           Sequence 11, Appl
    8      253   100.0     78  17  US-09-323-606C-4            Sequence 4, Appli
    9      253   100.0     78  23  US-09-928-047B-4            Sequence 4, Appli
   10      253   100.0     80  17  US-09-323-606C-10           Sequence 10, Appl
   11      253   100.0     82  17  US-09-323-606C-2            Sequence 2, Appli
   12      253   100.0     82  20  US-09-636-530-4             Sequence 4, Appli
   13      253   100.0     82  23  US-09-928-047B-2            Sequence 2, Appli
   14      253   100.0     83  20  US-09-636-530-2             Sequence 2, Appli
   15      253   100.0     83  23  US-09-928-047B-1            Sequence 1, Appli
   16      253   100.0     83  23  US-09-928-048A-4            Sequence 4, Appli
   17      253   100.0     84  17  US-09-323-606C-1            Sequence 1, Appli
   18      253   100.0     84  20  US-09-636-530-1             Sequence 1, Appli
   19      253   100.0     84  23  US-09-928-047B-5            Sequence 5, Appli
   20      253   100.0     84  23  US-09-928-048A-3            Sequence 3, Appli
   21      248    98.0     51  17  US-09-344-639D-3            Sequence 3, Appli
   22      248    98.0     51  24  US-10-002-818-3             Sequence 3, Appli
   23      248    98.0     78  16  US-09-231-422D-6            Sequence 6, Appli
   24      248    98.0     78  17  US-09-344-639D-6            Sequence 6, Appli
   25      248    98.0     78  22  US-09-843-221A-12           Sequence 12, Appl
   26      248    98.0     82  17  US-09-344-639D-2            Sequence 2, Appli
   27      248    98.0     83  24  US-10-002-818-2             Sequence 2, Appli
   28      248    98.0     84   1  PCT-US02-21356-1            Sequence 1, Appli
   29      248    98.0     84   1  PCT-US98-20848-1            Sequence 1, Appli
   30      248    98.0     84   3  US-07-806-271-2             Sequence 2, Appli
   31      248    98.0     84   4  US-08-016-171-2             Sequence 2, Appli
   32      248    98.0     84   7  US-08-329-856-2             Sequence 2, Appli
   33      248    98.0     84   7  US-08-345-151A-16           Sequence 16, Appl
   34      248    98.0     84   7  US-08-350-530A-25           Sequence 25, Appl
   35      248    98.0     84   7  US-08-350-709-9             Sequence 9, Appli
   36      248    98.0     84   7  US-08-350-709B-9            Sequence 9, Appli
   37      248    98.0     84   9  US-08-586-768-1             Sequence 1, Appli
   38      248    98.0     84  15  US-09-169-786-1             Sequence 1, Appli
   39      248    98.0     84  15  US-09-169-786-1             Sequence 1, Appli
   40      248    98.0     84  16  US-09-231-422B-2            Sequence 2, Appli
   41      248    98.0     84  16  US-09-231-422D-2            Sequence 2, Appli
   42      248    98.0     84  17  US-09-344-639D-1            Sequence 1, Appli
   43      248    98.0     84  20  US-09-657-276-256           Sequence 256, App
   44      248    98.0     84  22  US-09-843-221A-10           Sequence 10, Appl
   45      248    98.0     84  22  US-09-898-398-1             Sequence 1, Appli


                                 ALIGNMENTS


RESULT 1
US-09-323-606C-3
; Sequence 3, Application US/09323606C
; GENERAL INFORMATION:
;  APPLICANT: Cantor, Thomas
;  TITLE OF INVENTION: PARATHYROID HORMONE ANTAGONISTS OR
;  TITLE OF INVENTION:  MODULATORS AND METHODS THEREFOR
;  FILE REFERENCE: 53221-20009.00
;  CURRENT APPLICATION NUMBER: US/09/323,606C
;  CURRENT FILING DATE:  1999-01-18
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 51
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-323-606C-3

  Query Match              100.0%;  Score 253;  DB 17;  Length 51;
  Best Local Similarity    100.0%;  Pred. No. 7.6e-25;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51


RESULT 2
US-09-636-530-3
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; Sequence 3, Application US/09636530
; GENERAL INFORMATION:
;  APPLICANT: Cantor, Thomas
;  TITLE OF INVENTION: PARATHYROID HORMONE ANTAGONISTS OR
;  TITLE OF INVENTION:  MODULATORS AND USES THEREFOR
;  FILE REFERENCE: 53221-20003.00
;  CURRENT APPLICATION NUMBER: US/09/636,530
;  CURRENT FILING DATE:  2000-08-10
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 51
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-636-530-3

  Query Match             100.0%;  Score 253;  DB 20;  Length 51;
  Best Local Similarity   100.0%;  Pred. No. 7.6e-25;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51

RESULT 3
US-09-928-047B-3
; Sequence 3, Application US/09928047B
; GENERAL INFORMATION:
;  APPLICANT: Cantor, Thomas
;  TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
;  TITLE OF INVENTION:  ANTAGONIST OR MODULATORS AND OSTEOPOROSIS
;  FILE REFERENCE: 53221-20002.00
;  CURRENT APPLICATION NUMBER: US/09/928,047B
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: US 60/224,446
;  PRIOR FILING DATE: 2000-08-10
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 51
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-928-047B-3

  Query Match             100.0%;  Score 253;  DB 23;  Length 51;
  Best Local Similarity   100.0%;  Pred. No. 7.6e-25;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51

RESULT 4
US-09-928-048A-5
; Sequence 5, Application US/09928048A
; GENERAL INFORMATION:
;  APPLICANT: Scantibodies Laboratory, Inc.
;  APPLICANT:  Cantor, Thomas L.
;  TITLE OF INVENTION: METHODS AND DEVICES FOR DIRECT
;  TITLE OF INVENTION:  DETERMINATION OF CYCLASE INHIBITING PARATHYROID HORMONE
;  FILE REFERENCE: 53221-20015.00
;  CURRENT APPLICATION NUMBER: US/09/928,048A
;  CURRENT FILING DATE:  2000-08-10
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 51
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-928-048A-5

  Query Match             100.0%;  Score 253;  DB 23;  Length 51;
  Best Local Similarity   100.0%;  Pred. No. 7.6e-25;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51

RESULT 5
US-09-636-530-5
; Sequence 5, Application US/09636530
; GENERAL INFORMATION:
;  APPLICANT: Cantor, Thomas
;  TITLE OF INVENTION: PARATHYROID HORMONE ANTAGONISTS OR
;  TITLE OF INVENTION:  MODULATORS AND USES THEREFOR
;  FILE REFERENCE: 53221-20003.00
;  CURRENT APPLICATION NUMBER: US/09/636,530
;  CURRENT FILING DATE:  2000-08-10
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 57
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-636-530-5

  Query Match             100.0%;  Score 253;  DB 20;  Length 57;
  Best Local Similarity   100.0%;  Pred. No. 8.8e-25;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        7 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 57

RESULT 6
US-09-928-047B-8
; Sequence 8, Application US/09928047B
; GENERAL INFORMATION:
;  APPLICANT: Cantor, Thomas
;  TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
;  TITLE OF INVENTION:  ANTAGONIST OR MODULATORS AND OSTEOPOROSIS
;  FILE REFERENCE: 53221-20002.00
;  CURRENT APPLICATION NUMBER: US/09/928,047B
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: US 60/224,446
;  PRIOR FILING DATE: 2000-08-10
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 57
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-928-047B-8

  Query Match             100.0%;  Score 253;  DB 23;  Length 57;
  Best Local Similarity   100.0%;  Pred. No. 8.8e-25;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        7 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 57

RESULT 7
US-09-323-606C-11
; Sequence 11, Application US/09323606C
; GENERAL INFORMATION:
;  APPLICANT: Cantor, Thomas
;  TITLE OF INVENTION: PARATHYROID HORMONE ANTAGONISTS OR
;  TITLE OF INVENTION:  MODULATORS AND METHODS THEREFOR
;  FILE REFERENCE: 53221-20009.00
```

```
;  CURRENT APPLICATION NUMBER: US/09/323,606C
;  CURRENT FILING DATE:  1999-01-18
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 67
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-323-606C-11

  Query Match             100.0%;  Score 253;  DB 17;  Length 67;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-24;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       17 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 67


RESULT 8
US-09-323-606C-4
; Sequence 4, Application US/09323606C
; GENERAL INFORMATION:
;  APPLICANT: Cantor, Thomas
;  TITLE OF INVENTION: PARATHYROID HORMONE ANTAGONISTS OR
;  TITLE OF INVENTION:  MODULATORS AND METHODS THEREFOR
;  FILE REFERENCE: 53221-20009.00
;  CURRENT APPLICATION NUMBER: US/09/323,606C
;  CURRENT FILING DATE:  1999-01-18
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 78
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-323-606C-4

  Query Match             100.0%;  Score 253;  DB 17;  Length 78;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-24;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       28 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 78

RESULT 9
US-09-928-047B-4
; Sequence 4, Application US/09928047B
; GENERAL INFORMATION:
;  APPLICANT: Cantor, Thomas
;  TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
;  TITLE OF INVENTION:  ANTAGONIST OR MODULATORS AND OSTEOPOROSIS
;  FILE REFERENCE: 53221-20002.00
;  CURRENT APPLICATION NUMBER: US/09/928,047B
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: US 60/224,446
;  PRIOR FILING DATE: 2000-08-10
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 78
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-928-047B-4

  Query Match             100.0%;  Score 253;  DB 23;  Length 78;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-24;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       28 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 78
```

```
RESULT 10
US-09-323-606C-10
; Sequence 10, Application US/09323606C
; GENERAL INFORMATION:
;  APPLICANT: Cantor, Thomas
;  TITLE OF INVENTION: PARATHYROID HORMONE ANTAGONISTS OR
;  TITLE OF INVENTION:  MODULATORS AND METHODS THEREFOR
;  FILE REFERENCE: 53221-20009.00
;  CURRENT APPLICATION NUMBER: US/09/323,606C
;  CURRENT FILING DATE:  1999-01-18
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
;   LENGTH: 80
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-323-606C-10

  Query Match             100.0%;  Score 253;  DB 17;  Length 80;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-24;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       30 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 80

RESULT 11
US-09-323-606C-2
; Sequence 2, Application US/09323606C
; GENERAL INFORMATION:
;  APPLICANT: Cantor, Thomas
;  TITLE OF INVENTION: PARATHYROID HORMONE ANTAGONISTS OR
;  TITLE OF INVENTION:  MODULATORS AND METHODS THEREFOR
;  FILE REFERENCE: 53221-20009.00
;  CURRENT APPLICATION NUMBER: US/09/323,606C
;  CURRENT FILING DATE:  1999-01-18
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 82
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-323-606C-2

  Query Match             100.0%;  Score 253;  DB 17;  Length 82;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-24;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       32 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 82

RESULT 12
US-09-636-530-4
; Sequence 4, Application US/09636530
; GENERAL INFORMATION:
;  APPLICANT: Cantor, Thomas
;  TITLE OF INVENTION: PARATHYROID HORMONE ANTAGONISTS OR
;  TITLE OF INVENTION:  MODULATORS AND USES THEREFOR
;  FILE REFERENCE: 53221-20003.00
;  CURRENT APPLICATION NUMBER: US/09/636,530
;  CURRENT FILING DATE:  2000-08-10
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 82
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-636-530-4
```

```
  Query Match             100.0%;  Score 253;  DB 20;  Length 82;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-24;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       32 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 82


RESULT 13
US-09-928-047B-2
; Sequence 2, Application US/09928047B
; GENERAL INFORMATION:
;  APPLICANT: Cantor, Thomas
;  TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
;  TITLE OF INVENTION:  ANTAGONIST OR MODULATORS AND OSTEOPOROSIS
;  FILE REFERENCE: 53221-20002.00
;  CURRENT APPLICATION NUMBER: US/09/928,047B
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: US 60/224,446
;  PRIOR FILING DATE: 2000-08-10
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 82
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-928-047B-2

  Query Match             100.0%;  Score 253;  DB 23;  Length 82;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-24;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       32 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 82


RESULT 14
US-09-636-530-2
; Sequence 2, Application US/09636530
; GENERAL INFORMATION:
;  APPLICANT: Cantor, Thomas
;  TITLE OF INVENTION: PARATHYROID HORMONE ANTAGONISTS OR
;  TITLE OF INVENTION:  MODULATORS AND USES THEREFOR
;  FILE REFERENCE: 53221-20003.00
;  CURRENT APPLICATION NUMBER: US/09/636,530
;  CURRENT FILING DATE:  2000-08-10
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 83
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-636-530-2

  Query Match             100.0%;  Score 253;  DB 20;  Length 83;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-24;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       33 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 83


RESULT 15
US-09-928-047B-1
; Sequence 1, Application US/09928047B
; GENERAL INFORMATION:
;  APPLICANT: Cantor, Thomas
;  TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
;  TITLE OF INVENTION:  ANTAGONIST OR MODULATORS AND OSTEOPOROSIS
;  FILE REFERENCE: 53221-20002.00
;  CURRENT APPLICATION NUMBER: US/09/928,047B
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: US 60/224,446
;  PRIOR FILING DATE: 2000-08-10
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 83
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-928-047B-1

  Query Match             100.0%;  Score 253;  DB 23;  Length 83;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-24;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       33 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 83

Search completed: March 13, 2003, 14:57:47
Job time : 108.47 secs
```

```
                    GenCore version 5.1.4_p5_4578
             Copyright (c) 1993 - 2003  Compugen Ltd.


OM protein - protein search, using sw model

Run on:         March 13, 2003, 14:49:19 ; Search time 18.2687 Seconds
                                           (without alignments)
                                           362.927 Million cell updates/sec

Title:          US-09-636-530-3
Perfect score:  253
Sequence:       1 FVALGAPLAPRDAGSQRPRK..........KSLGEANKADVNVLTKAKSQ 51

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       596842 seqs, 130003698 residues

Total number of hits satisfying chosen parameters:      596842

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Pending_Patents_AA_New:*
                1:  /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*
                2:  /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
                3:  /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
                4:  /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
                5:  /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
                6:  /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*
                7:  /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                              SUMMARIES
                  %
Result          Query
  No.   Score   Match Length DB  ID                          Description
-----------------------------------------------------------------------------
    1     253   100.0     78  5  US-09-231-422F-6            Sequence 6, Appli
    2     253   100.0     84  1  PCT-US02-25348-1            Sequence 1, Appli
    3     253   100.0     84  5  US-09-231-422F-2            Sequence 2, Appli
    4     253   100.0     84  6  US-10-215-770-1             Sequence 1, Appli
    5     248    98.0     84  1  PCT-US02-40891-505          Sequence 505, App
    6     248    98.0     84  1  PCT-US02-40891-508          Sequence 508, App
    7     248    98.0     84  1  PCT-US02-40891-530          Sequence 530, App
    8     248    98.0     84  1  PCT-US02-40891-531          Sequence 531, App
    9     248    98.0     84  1  PCT-US02-40891-532          Sequence 532, App
   10     248    98.0     84  1  PCT-US02-40891-626          Sequence 626, App
   11     248    98.0     84  1  PCT-US03-02155-13           Sequence 13, Appl
   12     248    98.0     84  5  US-09-383-590-1             Sequence 1, Appli
   13     248    98.0     84  6  US-10-224-522-1             Sequence 1, Appli
   14     248    98.0     84  6  US-10-311-366-10            Sequence 10, Appl
   15     248    98.0    692  1  PCT-US02-40891-289          Sequence 289, App
   16     248    98.0    692  1  PCT-US02-40891-292          Sequence 292, App
   17     248    98.0    693  1  PCT-US02-40891-314          Sequence 314, App
   18     248    98.0    693  1  PCT-US02-40891-315          Sequence 315, App
   19     248    98.0    693  1  PCT-US02-40891-316          Sequence 316, App
   20     248    98.0    693  1  PCT-US02-40891-410          Sequence 410, App
   21     206    81.4     84  1  PCT-US02-25348-3            Sequence 3, Appli
   22     206    81.4     84  6  US-10-215-770-3             Sequence 3, Appli
   23     199    78.7     84  1  PCT-US02-25348-4            Sequence 4, Appli
   24     199    78.7     84  6  US-10-311-366-2             Sequence 2, Appli
   25     199    78.7     84  6  US-10-215-770-4             Sequence 4, Appli
   26     194    76.7     84  1  PCT-US02-25348-2            Sequence 2, Appli
```

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   27     194    76.7     84  6  US-10-215-770-2             Sequence 2, Appli
   28     164    64.8     84  6  US-10-311-366-11            Sequence 11, Appl
   29     160    63.2     84  1  PCT-US02-25348-5            Sequence 5, Appli
   30     160    63.2     84  6  US-10-215-770-5             Sequence 5, Appli
   31     151    59.7     32  6  US-10-311-366-27            Sequence 27, Appl
   32      97    38.3     22  6  US-10-311-366-3             Sequence 3, Appli
   33      95    37.5     21  6  US-10-311-366-4             Sequence 4, Appli
   34      84    33.2     91  7  US-60-443-566-2959          Sequence 2959, Ap
   35      84    33.2    123  7  US-60-443-566-2960          Sequence 2960, Ap
   36      75    29.6     21  6  US-10-311-366-26            Sequence 26, Appl
   37      75    29.6     22  6  US-10-311-366-25            Sequence 25, Appl
   38    68.5    27.1     88  1  PCT-US02-25348-6            Sequence 6, Appli
   39    68.5    27.1     88  6  US-10-215-770-6             Sequence 6, Appli
   40      66    26.1     15  6  US-10-311-366-6             Sequence 6, Appli
   41      66    26.1     16  6  US-10-311-366-5             Sequence 5, Appli
   42      61    24.1    565  6  US-10-282-122A-43871        Sequence 43871, A
   43      61    24.1    566  6  US-10-282-287-4             Sequence 4, Appli
   44      60    23.7   1942  6  US-10-144-779-422           Sequence 422, App
   45      59    23.3    130  1  PCT-US02-32727-13961        Sequence 13961, A


                              ALIGNMENTS


RESULT 1
US-09-231-422F-6
; Sequence 6, Application US/09231422F
; GENERAL INFORMATION:
;  APPLICANT: Scantibodies Laboratory, Inc.
;  APPLICANT: Cantor, Thomas
;  APPLICANT: Gao, Ping
;  TITLE OF INVENTION: METHODS, KITS AND ANTIBODIES FOR DETECTING
;  TITLE OF INVENTION: PARATHYROID HORMONE
;  FILE REFERENCE: 53221-20006.00
;  CURRENT APPLICATION NUMBER: US/09/231,422F
;  CURRENT FILING DATE:  1999-01-14
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 78
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-231-422F-6

  Query Match             100.0%;  Score 253;  DB 5;  Length 78;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-22;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
                |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         28 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 78


RESULT 2
PCT-US02-25348-1
; Sequence 1, Application PC/TUS0225348
; GENERAL INFORMATION:
;  APPLICANT: Cantor, Thomas L.
;  TITLE OF INVENTION: PARATHYROID HORMONE ANTAGONISTS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 53221-20002.40
;  CURRENT APPLICATION NUMBER: PCT/US02/25348
;  CURRENT FILING DATE:  2002-08-09
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 84
;   TYPE: PRT
;   ORGANISM: Homo sapiens
PCT-US02-25348-1

  Query Match             100.0%;  Score 253;  DB 1;  Length 84;
  Best Local Similarity   100.0%;  Pred. No. 2e-22;
```

```
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     34 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 84


RESULT 3
US-09-231-422F-2
; Sequence 2, Application US/09231422F
; GENERAL INFORMATION:
;  APPLICANT: Scantibodies Laboratory, Inc.
;  APPLICANT:  Cantor, Thomas
;  APPLICANT:  Gao, Ping
;  TITLE OF INVENTION: METHODS, KITS AND ANTIBODIES FOR DETECTING
;  TITLE OF INVENTION:  PARATHYROID HORMONE
;  FILE REFERENCE: 53221-20006.00
;  CURRENT APPLICATION NUMBER: US/09/231,422F
;  CURRENT FILING DATE:  1999-01-14
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 84
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-231-422F-2

  Query Match             100.0%;  Score 253;  DB 5;  Length 84;
  Best Local Similarity   100.0%;  Pred. No. 2e-22;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     34 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 84


RESULT 4
US-10-215-770-1
; Sequence 1, Application US/10215770
; GENERAL INFORMATION:
;  APPLICANT: Cantor, Thomas L.
;  TITLE OF INVENTION: PARATHYROID HORMONE ANTAGONISTS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 53221-20002.20
;  CURRENT APPLICATION NUMBER: US/10/215,770
;  CURRENT FILING DATE:  2002-12-16
;  PRIOR APPLICATION NUMBER: US 60/224,446
;  PRIOR FILING DATE: 2000-08-10
;  PRIOR APPLICATION NUMBER: US 60/224,447
;  PRIOR FILING DATE: 2000-08-10
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 84
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-215-770-1

  Query Match             100.0%;  Score 253;  DB 6;  Length 84;
  Best Local Similarity   100.0%;  Pred. No. 2e-22;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     34 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 84


RESULT 5
PCT-US02-40891-505
; Sequence 505, Application PC/TUS0240891
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc.
;  TITLE OF INVENTION: Albumin Fusion Proteins
;  FILE REFERENCE: PF564PCT
;  CURRENT APPLICATION NUMBER: PCT/US02/40891
;  CURRENT FILING DATE:  2002-12-23
;  PRIOR APPLICATION NUMBER: 60/341,811
;  PRIOR FILING DATE: 2001-12-21
;  PRIOR APPLICATION NUMBER: 60/360,000
;  PRIOR FILING DATE: 2002-02-28
;  PRIOR APPLICATION NUMBER: 60/378,950
;  PRIOR FILING DATE: 2002-05-10
;  PRIOR APPLICATION NUMBER: 60/398,008
;  PRIOR FILING DATE: 2002-07-24
;  PRIOR APPLICATION NUMBER: 60/411,355
;  PRIOR FILING DATE: 2002-09-18
;  PRIOR APPLICATION NUMBER: 60/414,984
;  PRIOR FILING DATE: 2002-10-02
;  PRIOR APPLICATION NUMBER: 60/417,611
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/420,246
;  PRIOR FILING DATE: 2002-10-23
;  PRIOR APPLICATION NUMBER: 60/423,623
;  PRIOR FILING DATE: 2002-11-05
;  PRIOR APPLICATION NUMBER: 60/351,360
;  PRIOR FILING DATE: 2002-01-28
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 2222
;  SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 505
;   LENGTH: 84
;   TYPE: PRT
;   ORGANISM: Homo sapiens
PCT-US02-40891-505

  Query Match             98.0%;  Score 248;  DB 1;  Length 84;
  Best Local Similarity   98.0%;  Pred. No. 7.7e-22;
  Matches   50;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
          |||||||||||||||||||||||||||||||||||||:|||||||||||||
Db     34 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEADKADVNVLTKAKSQ 84


RESULT 6
PCT-US02-40891-508
; Sequence 508, Application PC/TUS0240891
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc.
;  TITLE OF INVENTION: Albumin Fusion Proteins
;  FILE REFERENCE: PF564PCT
;  CURRENT APPLICATION NUMBER: PCT/US02/40891
;  CURRENT FILING DATE:  2002-12-23
;  PRIOR APPLICATION NUMBER: 60/341,811
;  PRIOR FILING DATE: 2001-12-21
;  PRIOR APPLICATION NUMBER: 60/360,000
;  PRIOR FILING DATE: 2002-02-28
;  PRIOR APPLICATION NUMBER: 60/378,950
;  PRIOR FILING DATE: 2002-05-10
;  PRIOR APPLICATION NUMBER: 60/398,008
;  PRIOR FILING DATE: 2002-07-24
;  PRIOR APPLICATION NUMBER: 60/411,355
;  PRIOR FILING DATE: 2002-09-18
;  PRIOR APPLICATION NUMBER: 60/414,984
;  PRIOR FILING DATE: 2002-10-02
;  PRIOR APPLICATION NUMBER: 60/417,611
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/420,246
;  PRIOR FILING DATE: 2002-10-23
;  PRIOR APPLICATION NUMBER: 60/423,623
;  PRIOR FILING DATE: 2002-11-05
;  PRIOR APPLICATION NUMBER: 60/351,360
;  PRIOR FILING DATE: 2002-01-28
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 2222
;  SOFTWARE: Patentin Ver. 2.0
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; SEQ ID NO 508
;   LENGTH: 84
;   TYPE: PRT
;   ORGANISM: Homo sapiens
PCT-US02-40891-508

  Query Match             98.0%;  Score 248;  DB 1;  Length 84;
  Best Local Similarity   98.0%;  Pred. No. 7.7e-22;
  Matches   50;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
             |||||||||||||||||||||||||||||||||||||:|||||||||||||
Db      34 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEADKADVNVLTKAKSQ 84


RESULT 7
PCT-US02-40891-530
; Sequence 530, Application PC/TUS0240891
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc.
;  TITLE OF INVENTION: Albumin Fusion Proteins
;  FILE REFERENCE: PF564PCT
;  CURRENT APPLICATION NUMBER: PCT/US02/40891
;  CURRENT FILING DATE:  2002-12-23
;  PRIOR APPLICATION NUMBER: 60/341,811
;  PRIOR FILING DATE: 2001-12-21
;  PRIOR APPLICATION NUMBER: 60/360,000
;  PRIOR FILING DATE: 2002-02-28
;  PRIOR APPLICATION NUMBER: 60/378,950
;  PRIOR FILING DATE: 2002-05-10
;  PRIOR APPLICATION NUMBER: 60/398,008
;  PRIOR FILING DATE: 2002-07-24
;  PRIOR APPLICATION NUMBER: 60/411,355
;  PRIOR FILING DATE: 2002-09-18
;  PRIOR APPLICATION NUMBER: 60/414,984
;  PRIOR FILING DATE: 2002-10-02
;  PRIOR APPLICATION NUMBER: 60/417,611
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/420,246
;  PRIOR FILING DATE: 2002-10-23
;  PRIOR APPLICATION NUMBER: 60/423,623
;  PRIOR FILING DATE: 2002-11-05
;  PRIOR APPLICATION NUMBER: 60/351,360
;  PRIOR FILING DATE: 2002-01-28
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 2222
;  SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 530
;   LENGTH: 84
;   TYPE: PRT
;   ORGANISM: Homo sapiens
PCT-US02-40891-530

  Query Match             98.0%;  Score 248;  DB 1;  Length 84;
  Best Local Similarity   98.0%;  Pred. No. 7.7e-22;
  Matches   50;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
             |||||||||||||||||||||||||||||||||||||:|||||||||||||
Db      34 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEADKADVNVLTKAKSQ 84


RESULT 8
PCT-US02-40891-531
; Sequence 531, Application PC/TUS0240891
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc.
;  TITLE OF INVENTION: Albumin Fusion Proteins
;  FILE REFERENCE: PF564PCT
;  CURRENT APPLICATION NUMBER: PCT/US02/40891
;  CURRENT FILING DATE:  2002-12-23
;  PRIOR APPLICATION NUMBER: 60/341,811
;  PRIOR FILING DATE: 2001-12-21
;  PRIOR APPLICATION NUMBER: 60/360,000
;  PRIOR FILING DATE: 2002-02-28
;  PRIOR APPLICATION NUMBER: 60/378,950
;  PRIOR FILING DATE: 2002-05-10
;  PRIOR APPLICATION NUMBER: 60/398,008
;  PRIOR FILING DATE: 2002-07-24
;  PRIOR APPLICATION NUMBER: 60/411,355
;  PRIOR FILING DATE: 2002-09-18
;  PRIOR APPLICATION NUMBER: 60/414,984
;  PRIOR FILING DATE: 2002-10-02
;  PRIOR APPLICATION NUMBER: 60/417,611
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/420,246
;  PRIOR FILING DATE: 2002-10-23
;  PRIOR APPLICATION NUMBER: 60/423,623
;  PRIOR FILING DATE: 2002-11-05
;  PRIOR APPLICATION NUMBER: 60/351,360
;  PRIOR FILING DATE: 2002-01-28
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 2222
;  SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 531
;   LENGTH: 84
;   TYPE: PRT
;   ORGANISM: Homo sapiens
PCT-US02-40891-531

  Query Match             98.0%;  Score 248;  DB 1;  Length 84;
  Best Local Similarity   98.0%;  Pred. No. 7.7e-22;
  Matches   50;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
             |||||||||||||||||||||||||||||||||||||:|||||||||||||
Db      34 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEADKADVNVLTKAKSQ 84


RESULT 9
PCT-US02-40891-532
; Sequence 532, Application PC/TUS0240891
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc.
;  TITLE OF INVENTION: Albumin Fusion Proteins
;  FILE REFERENCE: PF564PCT
;  CURRENT APPLICATION NUMBER: PCT/US02/40891
;  CURRENT FILING DATE:  2002-12-23
;  PRIOR APPLICATION NUMBER: 60/341,811
;  PRIOR FILING DATE: 2001-12-21
;  PRIOR APPLICATION NUMBER: 60/360,000
;  PRIOR FILING DATE: 2002-02-28
;  PRIOR APPLICATION NUMBER: 60/378,950
;  PRIOR FILING DATE: 2002-05-10
;  PRIOR APPLICATION NUMBER: 60/398,008
;  PRIOR FILING DATE: 2002-07-24
;  PRIOR APPLICATION NUMBER: 60/411,355
;  PRIOR FILING DATE: 2002-09-18
;  PRIOR APPLICATION NUMBER: 60/414,984
;  PRIOR FILING DATE: 2002-10-02
;  PRIOR APPLICATION NUMBER: 60/417,611
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/420,246
;  PRIOR FILING DATE: 2002-10-23
;  PRIOR APPLICATION NUMBER: 60/423,623
;  PRIOR FILING DATE: 2002-11-05
;  PRIOR APPLICATION NUMBER: 60/351,360
;  PRIOR FILING DATE: 2002-01-28
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 2222
;  SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 532
;   LENGTH: 84
;   TYPE: PRT
;   ORGANISM: Homo sapiens
PCT-US02-40891-532
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  Query Match             98.0%;  Score 248;  DB 1;  Length 84;
  Best Local Similarity   98.0%;  Pred. No. 7.7e-22;
  Matches   50;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
              |||||||||||||||||||||||||||||||||||||:|||||||||||||
Db         34 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEADKADVNVLTKAKSQ 84


RESULT 10
PCT-US02-40891-626
; Sequence 626, Application PC/TUS0240891
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc.
;  TITLE OF INVENTION: Albumin Fusion Proteins
;  FILE REFERENCE: PF564PCT
;  CURRENT APPLICATION NUMBER: PCT/US02/40891
;  CURRENT FILING DATE:  2002-12-23
;  PRIOR APPLICATION NUMBER: 60/341,811
;  PRIOR FILING DATE: 2001-12-21
;  PRIOR APPLICATION NUMBER: 60/360,000
;  PRIOR FILING DATE: 2002-02-28
;  PRIOR APPLICATION NUMBER: 60/378,950
;  PRIOR FILING DATE: 2002-05-10
;  PRIOR APPLICATION NUMBER: 60/398,008
;  PRIOR FILING DATE: 2002-07-24
;  PRIOR APPLICATION NUMBER: 60/411,355
;  PRIOR FILING DATE: 2002-09-18
;  PRIOR APPLICATION NUMBER: 60/414,984
;  PRIOR FILING DATE: 2002-10-02
;  PRIOR APPLICATION NUMBER: 60/417,611
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/420,246
;  PRIOR FILING DATE: 2002-10-23
;  PRIOR APPLICATION NUMBER: 60/423,623
;  PRIOR FILING DATE: 2002-11-05
;  PRIOR APPLICATION NUMBER: 60/351,360
;  PRIOR FILING DATE: 2002-01-28
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 2222
;  SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 626
;   LENGTH: 84
;   TYPE: PRT
;   ORGANISM: Homo sapiens
PCT-US02-40891-626

  Query Match             98.0%;  Score 248;  DB 1;  Length 84;
  Best Local Similarity   98.0%;  Pred. No. 7.7e-22;
  Matches   50;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
              |||||||||||||||||||||||||||||||||||||:|||||||||||||
Db         34 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEADKADVNVLTKAKSQ 84


RESULT 11
PCT-US03-02155-13
; Sequence 13, Application PC/TUS0302155
; GENERAL INFORMATION:
;  APPLICANT: Gardella, Thomas J.
;  APPLICANT:  Kronenberg, Henry M.
;  APPLICANT:  Potts, John T.
;  TITLE OF INVENTION: Conformationally Constrained Parathyroid Hormone (PTH) Analogs
;  TITLE OF INVENTION:  With Lactam Bridges
;  FILE REFERENCE: 0609.514PC00
;  CURRENT APPLICATION NUMBER: PCT/US03/02155
;  CURRENT FILING DATE:  2003-01-24
;  NUMBER OF SEQ ID NOS: 37
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
;   LENGTH: 84
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (84)..(84)
;   OTHER INFORMATION: AMIDATION
PCT-US03-02155-13

  Query Match             98.0%;  Score 248;  DB 1;  Length 84;
  Best Local Similarity   98.0%;  Pred. No. 7.7e-22;
  Matches   50;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
              |||||||||||||||||||||||||||||||||||||:|||||||||||||
Db         34 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEADKADVNVLTKAKSQ 84


RESULT 12
US-09-383-590-1
; Sequence 1, Application US/09383590
; GENERAL INFORMATION:
;  APPLICANT: Backstrom, Kjell G. E.
;  APPLICANT:  Wallmark, Bjorn
;  APPLICANT:  Dahlback, Magnus
;  APPLICANT:  Edman, Peter
;  APPLICANT:  Johansson, Ann
;  TITLE OF INVENTION: THERAPEUTIC PREPARATIONS FOR INHALATION
;  FILE REFERENCE: 06275-110002
;  CURRENT APPLICATION NUMBER: US/09/383,590
;  CURRENT FILING DATE:  1999-08-26
;  PRIOR APPLICATION NUMBER: US 08/586,768
;  PRIOR FILING DATE: 1996-01-30
;  PRIOR APPLICATION NUMBER: PCT/SE95/01475
;  PRIOR FILING DATE: 1995-12-08
;  PRIOR APPLICATION NUMBER: SE 9404449-2
;  PRIOR FILING DATE: 1994-12-22
;  PRIOR APPLICATION NUMBER: SE 9502576-3
;  PRIOR FILING DATE: 1995-07-12
;  NUMBER OF SEQ ID NOS: 1
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 84
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-383-590-1

  Query Match             98.0%;  Score 248;  DB 5;  Length 84;
  Best Local Similarity   98.0%;  Pred. No. 7.7e-22;
  Matches   50;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
              |||||||||||||||||||||||||||||||||||||:|||||||||||||
Db         34 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEADKADVNVLTKAKSQ 84


RESULT 13
US-10-224-522-1
; Sequence 1, Application US/10224522
; GENERAL INFORMATION:
;  APPLICANT: Backstrom, Kjell G. E.
;  APPLICANT:  Wallmark, Bjorn
;  APPLICANT:  Dahlbck, Magnus
;  APPLICANT:  Edman, Peter
;  APPLICANT:  Johansson, Ann
;  TITLE OF INVENTION: THERAPEUTIC PREPARATIONS FOR INHALATION
;  FILE REFERENCE: 06275-110003
;  CURRENT APPLICATION NUMBER: US/10/224,522
;  CURRENT FILING DATE:  2002-08-19
;  PRIOR APPLICATION NUMBER: US 09/383,590
;  PRIOR FILING DATE: 1999-08-26
;  PRIOR APPLICATION NUMBER: US 08/586,768
;  PRIOR FILING DATE: 1996-01-30
;  PRIOR APPLICATION NUMBER: PCT/SE95/01475
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;  PRIOR FILING DATE: 1995-12-08
;  PRIOR APPLICATION NUMBER: SE 9404449-2
;  PRIOR FILING DATE: 1994-12-22
;  PRIOR APPLICATION NUMBER: SE 9502576-3
;  PRIOR FILING DATE: 1995-07-12
;  NUMBER OF SEQ ID NOS: 1
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 84
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-224-522-1

  Query Match             98.0%;  Score 248;  DB 6;  Length 84;
  Best Local Similarity   98.0%;  Pred. No. 7.7e-22;
  Matches   50;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
             |||||||||||||||||||||||||||||||||||||:|||||||||||||
Db      34 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEADKADVNVLTKAKSQ 84


RESULT 14
US-10-311-366-10
; Sequence 10, Application US/10311366
; GENERAL INFORMATION:
;  APPLICANT: Holick, Michael F.
;  TITLE OF INVENTION: Regulation Of Cell Proliferation And Differentiation Using Topica
;  TITLE OF INVENTION:  Applied Peptides
;  FILE REFERENCE: 1539.0310001
;  CURRENT APPLICATION NUMBER: US/10/311,366
;  CURRENT FILING DATE:  2002-12-16
;  PRIOR APPLICATION NUMBER: PCT/US01/19650
;  PRIOR FILING DATE: 2001-06-20
;  PRIOR APPLICATION NUMBER: US 60/213,247
;  PRIOR FILING DATE: 2000-06-22
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
;   LENGTH: 84
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: hPTH
US-10-311-366-10

  Query Match             98.0%;  Score 248;  DB 6;  Length 84;
  Best Local Similarity   98.0%;  Pred. No. 7.7e-22;
  Matches   50;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
             |||||||||||||||||||||||||||||||||||||:|||||||||||||
Db      34 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEADKADVNVLTKAKSQ 84


RESULT 15
PCT-US02-40891-289
; Sequence 289, Application PC/TUS0240891
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc.
;  TITLE OF INVENTION: Albumin Fusion Proteins
;  FILE REFERENCE: PF564PCT
;  CURRENT APPLICATION NUMBER: PCT/US02/40891
;  CURRENT FILING DATE:  2002-12-23
;  PRIOR APPLICATION NUMBER: 60/341,811
;  PRIOR FILING DATE: 2001-12-21
;  PRIOR APPLICATION NUMBER: 60/360,000
;  PRIOR FILING DATE: 2002-02-28
;  PRIOR APPLICATION NUMBER: 60/378,950
;  PRIOR FILING DATE: 2002-05-10
;  PRIOR APPLICATION NUMBER: 60/398,008
;  PRIOR FILING DATE: 2002-07-24
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;  PRIOR APPLICATION NUMBER: 60/411,355
;  PRIOR FILING DATE: 2002-09-18
;  PRIOR APPLICATION NUMBER: 60/414,984
;  PRIOR FILING DATE: 2002-10-02
;  PRIOR APPLICATION NUMBER: 60/417,611
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/420,246
;  PRIOR FILING DATE: 2002-10-23
;  PRIOR APPLICATION NUMBER: 60/423,623
;  PRIOR FILING DATE: 2002-11-05
;  PRIOR APPLICATION NUMBER: 60/351,360
;  PRIOR FILING DATE: 2002-01-28
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 2222
;  SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 289
;   LENGTH: 692
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (532)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
PCT-US02-40891-289

  Query Match             98.0%;  Score 248;  DB 1;  Length 692;
  Best Local Similarity   98.0%;  Pred. No. 8e-21;
  Matches   50;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
             |||||||||||||||||||||||||||||||||||||:|||||||||||||
Db     642 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEADKADVNVLTKAKSQ 692


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Job time : 18.2687 secs
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                      GenCore version 5.1.4_p5_4578
              Copyright (c) 1993 - 2003  Compugen Ltd.

OM protein - protein search, using sw model

Run on:         March 13, 2003, 14:58:49 ; Search time 9.89552 Seconds
                                           (without alignments)
                                           495.462 Million cell updates/sec

Title:          US-09-636-530-3
Perfect score:  253
Sequence:       1 FVALGAPLAPRDAGSQRPRK..........KSLGEANKADVNVLTKAKSQ 51

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters:      283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       PIR_73:*
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                2:  pir2:*
                3:  pir3:*
                4:  pir4:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                                SUMMARIES
                      %
Result             Query
  No.    Score   Match Length DB  ID                  Description
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    2     206    81.4    115  2  JC4202              parathyroid hormon
    3     199    78.7    115  1  PTBO                parathyroid hormon
    4     194    76.7    115  1  PTPG                parathyroid hormon
    5     160    63.2    105  2  I51851              parathyroid hormon
    6     160    63.2    115  2  A05091              parathyroid hormon
    7    68.5    27.1    119  2  A34937              parathyroid hormon
    8      65    25.7    283  2  H86803              prophage pi3 prote
    9    63.5    25.1    487  2  A71407              probable Ste20-lik
   10      63    24.9   1937  2  I38055              myosin heavy chain
   11    61.5    24.3    366  2  A64028              hypothetical prote
   12      61    24.1    565  2  G89813              DNA polymerase III
   13    60.5    23.9    555  2  T44010              virion protein [im
   14      60    23.7    258  2  A02985              myosin heavy chain
   15      60    23.7    955  2  S24348              myosin heavy chain
   16      60    23.7   1938  2  A59293              skeletal myosin he
   17      60    23.7   1940  2  A29320              myosin heavy chain
   18      60    23.7   5170  2  T15348              hypothetical prote
   19    59.5    23.5   1400  2  T33758              hypothetical prote
   20      59    23.3    404  2  C64597              lipopolysacharide
   21    58.5    23.1    142  2  T45922              probable C2H2-type
   22      58    22.9    234  2  S33732              myosin alpha heavy
   23      58    22.9    465  2  A02986              myosin alpha heavy
   24      58    22.9   1038  1  MWRBCB              myosin beta heavy
   25      58    22.9   1935  1  A37102              myosin beta heavy
   26      58    22.9   1935  1  S06006              myosin beta heavy
   27      58    22.9   1935  2  A59286              myosin heavy chain
   28    57.5    22.7    378  2  F56653              virion protein - h
   29    56.5    22.3    655  2  C71438              hypothetical prote
   30    56.5    22.3    674  2  B71438              hypothetical prote
   31    56.5    22.3    727  2  T24284              hypothetical prote
   32      56    22.1    396  2  G96934              DNA-damage repair
   33      56    22.1   1787  2  G97222              hypothetical prote
   34      56    22.1   1931  2  A59234              slow myosin heavy
   35      56    22.1   1938  1  JX0178              myosin heavy chain
   36    55.5    21.9    412  2  T51080              hypothetical prote
   37    55.5    21.9   1203  2  S26650              DNA-binding protei
   38      55    21.7    269  2  T15500              hypothetical prote
   39      55    21.7    854  2  S02003              neurofilament trip
   40      55    21.7   1072  1  A37221              neurofilament trip
   41      55    21.7   1154  2  T18525              diacylglycerol kin
   42      55    21.7   1157  2  T19187              hypothetical prote
   43      55    21.7   1505  2  T31418              synaptonemal compl
   44      55    21.7   1518  2  S37928              probable purine nu
   45      55    21.7   1934  2  I48153              myosin heavy chain


                                ALIGNMENTS


RESULT 1
PTHU
parathyroid hormone precursor [validated] - human
N;Alternate names: proparathyroid hormone
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 19-Jan-1996 #text_change 08-Dec-2000
C;Accession: A19339; S53790; A93169; S21199; A93789; A93783; A90387; A90426; A94410;
R;Vasicek, T.J.; McDevitt, B.E.; Freeman, M.W.; Fennick, B.J.; Hendy, G.N.; Potts Jr.
Proc. Natl. Acad. Sci. U.S.A. 80, 2127-2131, 1983
A;Title: Nucleotide sequence of the human parathyroid hormone gene.
A;Reference number: A19339; MUID:83169834; PMID:6220408
A;Accession: A19339
A;Molecule type: DNA
A;Residues: 1-115 <VAS>
A;Cross-references: GB:J00301; NID:g190702; PIDN:AAA60215.1; PID:g190704
R;Yamaguchi, T.; Fukase, M.; Sugimoto, T.; Kido, H.; Chihara, K.
Biol. Chem. Hoppe-Seyler 375, 821-824, 1994
A;Title: Purification of meprin from human kidney and its role in parathyroid hormone
A;Reference number: S53790; MUID:95225988; PMID:7710697
A;Accession: S53790
A;Molecule type: protein
A;Residues: 'X',33,'X',35-46;65-84;105-110 <YAM>
A;Note: peptides generated in vitro and in vivo by meprin; peptide cleavage also occu
R;Jacobs, J.W.; Kemper, B.; Niall, H.D.; Habener, J.F.; Potts Jr., J.T.
Nature 249, 155-157, 1974
A;Title: Structural analysis of human proparathyroid hormone by a new microsequencing
A;Reference number: A93169; MUID:74174967; PMID:4833516
A;Accession: A93169
A;Molecule type: protein
A;Residues: 26-37 <JAC>
R;Olstad, O.K.; Reppe, S.; Gabrielsen, O.S.; Hartmanis, M.; Blingsmo, O.R.; Gautvik,
Eur. J. Biochem. 205, 311-319, 1992
A;Title: Isolation and characterization of two biologically active O-glycosylated for
ation.
A;Reference number: S21199; MUID:92209518; PMID:1555591
A;Accession: S21199
A;Molecule type: protein
A;Residues: 32-114,'N' <OLS>
A;Note: cloned sequence expressed in Saccharomyces cerevisiae exhibited O-glycosylati
R;Niall, H.D.; Sauer, R.T.; Jacobs, J.W.; Keutmann, H.T.; Segre, G.V.; O'Riordan, J.L
Proc. Natl. Acad. Sci. U.S.A. 71, 384-388, 1974
A;Title: The amino-acid sequence of the amino-terminal 37 residues of human parathyro
A;Reference number: A93789; MUID:74111656; PMID:4521809
A;Accession: A93789
A;Molecule type: protein
A;Residues: 32-68 <NIA>
R;Brewer Jr., H.B.; Fairwell, T.; Ronan, R.; Sizemore, G.W.; Arnaud, C.D.
Proc. Natl. Acad. Sci. U.S.A. 69, 3585-3588, 1972
A;Title: Human parathyroid hormone: amino-acid sequence of the amino-terminal residue
A;Reference number: A93783; MUID:73070429; PMID:4509319
A;Accession: A93783
A;Molecule type: protein
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A;Residues: 32-52,'Q',54-58,'K',60,'L',62-65 <BRE>
A;Note: this sequence was determined by sequenator and mass spectroscopic identificatio
R;Keutmann, H.T.; Niall, H.D.; O'Riordan, J.L.H.; Potts Jr., J.T.
Biochemistry 14, 1842-1847, 1975
A;Title: A reinvestigation of the amino-terminal sequence of human parathyroid hormone.
A;Reference number: A90387; MUID:75146516; PMID:1125201
A;Accession: A90387
A;Molecule type: protein
A;Residues: 52-75 <KE3>
R;Keutmann, H.T.; Sauer, M.M.; Hendy, G.N.; O'Riordan, J.L.H.; Potts Jr., J.T.
Biochemistry 17, 5723-5729, 1978
A;Title: Complete amino acid sequence of human parathyroid hormone.
A;Reference number: A90426; MUID:79082855; PMID:728431
A;Accession: A90426
A;Molecule type: protein
A;Residues: 61-106,'D',108-115 <KEU>
R;Keutmann, H.T.; Niall, H.D.; Jacobs, J.W.; Barling, P.M.; Hendy, G.N.; O'Riordan, J.L
in Calcium-regulating Hormones, Talmadge, R.V., Owen, M., and Parsons, J.A., eds., pp.9
A;Reference number: A94410
A;Accession: A94410
A;Molecule type: protein
A;Residues: 75-100 <KE2>
R;Tregear, G.W.; van Rietschoten, J.; Green, E.; Niall, H.D.; Keutmann, H.T.; Parsons,
Hoppe-Seyler's Z. Physiol. Chem. 355, 415-421, 1974
A;Title: Solid-phase synthesis of the biologically active N-terminal 1-34 peptide of hu
A;Reference number: A91660; MUID:75059220; PMID:4474131
A;Contents: annotation; synthesis of residues 32-65
A;Note: the biologically active amino-terminal 34 residues of parathyroid hormone were
at renal adenylate cyclase assay and with the bovine hormone's active region in the chi
R;Andreatta, R.H.; Hartmann, A.; Joehl, A.; Kamber, B.; Maier, R.; Riniker, B.; Rittel,
Helv. Chim. Acta 56, 470-473, 1973
A;Title: Synthese der Sequenz 1-34 von menschlichem Parat-hormon.
A;Reference number: A91635; MUID:73227467; PMID:4721748
A;Contents: annotation; synthesis of residues 32-65
A;Note: the amino-terminal 34 residues of the parathyroid hormone sequence as determine
 into thyroparathyroidectomized rats caused a distinct increase in plasma calcium level
R;Hendy, G.N.; Kronenberg, H.M.; Potts, J.T.
Proc. Natl. Acad. Sci. U.S.A. 78, 7365-7369, 1981
A;Title: Nucleotide sequence of cloned cDNAs encoding human preproparathyroid hormone.
A;Reference number: I38342; MUID:82150870; PMID:6950381
A;Accession: I38342
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-115 <RES>
A;Cross-references: EMBL:V00597; NID:g37143; PIDN:CAA23843.1; PID:g37144
C;Genetics:
A;Gene: GDB:PTH
A;Cross-references: GDB:119522; OMIM:168450
A;Map position: 11p15.2-11p15.1
A;Introns: 29/2
A;Note: the first intron occurs before the initiator codon
C;Function:
A;Description: factor in homeostatic control of plasma calcium and phosphate; released
 counter to calcitonin
C;Superfamily: parathyroid hormone; parathyroid hormone homology
C;Keywords: calcium; hormone; parathyroid gland; plasma
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-31/Domain: propeptide #status experimental <PRO>
F;30-64/Domain: parathyroid hormone homology <PTH>
F;32-115/Product: parathyroid hormone #status experimental <MAT>

  Query Match             98.0%;  Score 248;  DB 1;  Length 115;
  Best Local Similarity   98.0%;  Pred. No. 7e-23;
  Matches   50;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
          |||||||||||||||||||||||||||||||||||||:|||||||||||||
Db     65 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEADKADVNVLTKAKSQ 115


RESULT 2
JC4202
parathyroid hormone precursor - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 10-Sep-1995 #sequence_revision 27-Oct-1995 #text_change 16-Jul-1999
C;Accession: JC4202
R;Rosol, T.J.; Steinmeyer, C.L.; McCauley, L.K.; Groene, A.; DeWille, J.W.; Capen, C.
Gene 160, 241-243, 1995
A;Title: Sequences of the cDNAs encoding canine parathyroid hormone-related protein a
A;Reference number: JC4201; MUID:95369696; PMID:7642102
A;Accession: JC4202
A;Molecule type: mRNA
A;Residues: 1-115 <ROS>
A;Cross-references: GB:U15662; NID:g558915; PIDN:AAA82584.1; PID:g558916
C;Superfamily: parathyroid hormone; parathyroid hormone homology
C;Keywords: hormone
F;1-31/Domain: signal sequence #status predicted <SIG>
F;30-64/Domain: parathyroid hormone homology <PTH>
F;32-115/Product: parathyroid hormone #status predicted <MAT>

  Query Match             81.4%;  Score 206;  DB 2;  Length 115;
  Best Local Similarity   82.4%;  Pred. No. 8.5e-18;
  Matches   42;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
          |||||||:| ||  |||| ||||||||||::||||||:||||:||||||||
Db     65 FVALGAPIAHRDGSSQRPLKKEDNVLVESYQKSLGEADKADVDVLTKAKSQ 115


RESULT 3
PTBO
parathyroid hormone precursor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 18-Jun-1999
C;Accession: A24949; A93835; A93793; A91648; A93773; I45975; I45976; A01534
R;Weaver, C.A.; Gordon, D.F.; Kissil, M.S.; Mead, D.A.; Kemper, B.
Gene 28, 319-329, 1984
A;Title: Isolation and complete nucleotide sequence of the gene for bovine parathyroi
A;Reference number: A24949; MUID:84262483; PMID:6086460
A;Accession: A24949
A;Molecule type: DNA
A;Residues: 1-115 <WEA>
A;Cross-references: GB:K01938
R;Kronenberg, H.M.; McDevitt, B.E.; Majzoub, J.A.; Nathans, J.; Sharp, P.A.; Potts Jr
Proc. Natl. Acad. Sci. U.S.A. 76, 4981-4985, 1979
A;Title: Cloning and nucleotide sequence of DNA coding for bovine preproparathyroid h
A;Reference number: A93835; MUID:80056617; PMID:388425
A;Accession: A93835
A;Molecule type: DNA
A;Residues: 1-115 <KRO>
A;Cross-references: GB:V00106; GB:J00023; NID:g84; PIDN:CAA23439.1; PID:g85
A;Note: the authors translated the codon GAA for residue 50 as Gly
R;Hamilton, J.W.; Niall, H.D.; Jacobs, J.W.; Keutmann, H.T.; Potts Jr., J.T.; Cohn, D
Proc. Natl. Acad. Sci. U.S.A. 71, 653-656, 1974
A;Title: The N-terminal amino-acid sequence of bovine proparathyroid hormone.
A;Reference number: A93793; MUID:74142666; PMID:4522780
A;Accession: A93793
A;Molecule type: protein
A;Residues: 26-115 <HAM>
R;Niall, H.D.; Keutmann, H.T.; Sauer, R.; Hogan, M.L.; Dawson, B.F.; Aurbach, G.D.; P
Hoppe-Seyler's Z. Physiol. Chem. 351, 1586-1588, 1970
A;Title: The amino acid sequence of bovine parathyroid hormone I.
A;Reference number: A91648; MUID:71076162; PMID:5531031
A;Accession: A91648
A;Molecule type: protein
A;Residues: 32-115 <NIA>
R;Brewer Jr., H.B.; Ronan, R.
Proc. Natl. Acad. Sci. U.S.A. 67, 1862-1869, 1970
A;Title: Bovine parathyroid hormone: amino acid sequence.
A;Reference number: A93773; MUID:71063634; PMID:5275384
A;Accession: A93773
A;Molecule type: protein
A;Residues: 32-115 <BRE>
R;Potts Jr., J.T.; Tregear, G.W.; Keutmann, H.T.; Niall, H.D.; Sauer, R.; Deftos, L.J
Proc. Natl. Acad. Sci. U.S.A. 68, 63-67, 1971
A;Title: Synthesis of a biologically active N-terminal tetratriacontapeptide of parat
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A;Reference number: A93776; MUID:71091588; PMID:4322265
A;Contents: annotation; synthesis of residues 32-65
A;Note: the synthetic peptide was active in vivo and in vitro
R;Brewer Jr., H.B.; Fairwell, T.; Rittel, W.; Littledike, T.; Arnaud, C.D.
Am. J. Med. 56, 759-766, 1974
A;Title: Recent studies on the chemistry of human, bovine and porcine parathyroid hormon
A;Reference number: A90030; MUID:74173303; PMID:4598526
A;Contents: annotation
R;Weaver, C.A.; Gordon, D.F.
Proc. Natl. Acad. Sci. U.S.A. 78, 4073-4077, 1981
A;Title: introduction by molecular cloning of artifactual inverted sequences at the 5' t
A;Reference number: I45975; MUID:82037785; PMID:6170060
A;Accession: I45975
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-115 <WE2>
A;Cross-references: GB:J00024; NID:g163642; PIDN:AAA30747.1; PID:g163643
R;Weaver, C.A.; Gordon, D.F.
Mol. Cell. Endocrinol. 28, 411-424, 1982
A;Title: Nucleotide sequence of bovine parathyroid hormone messenger RNA.
A;Reference number: I45976; MUID:83105964; PMID:6185374
A;Accession: I45976
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-115 <WE3>
A;Cross-references: GB:M25082; NID:g163644; PIDN:AAA30748.1; PID:g163645
C;Genetics:
A;Gene: PTH
A;Introns: 29/2
C;Superfamily: parathyroid hormone; parathyroid hormone homology
C;Keywords: hormone
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-115/Product: proparathyroid hormone #status experimental <PMAT>
F;26-31/Domain: propeptide #status experimental <PRO>
F;30-64/Domain: parathyroid hormone homology <PTH>
F;32-115/Product: parathyroid hormone #status experimental <MAT>

  Query Match             78.7%;  Score 199;  DB 1;  Length 115;
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  Matches   41;  Conservative    4;  Mismatches    6;  Indels    0;  Gaps    0;

Qy        1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
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Db       65 FVALGASIAYRDGSSQRPRKKEDNVLVESHQKSLGEADKADVDVLIKAKPQ 115


RESULT 4
PTPG
parathyroid hormone precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 24-Apr-1984 #sequence_revision 12-Apr-1996 #text_change 18-Jun-1999
C;Accession: B26806; A90390; A90376; A01535
R;Schmelzer, H.J.; Gross, G.; Widera, G.; Mayer, H.
Nucleic Acids Res. 15, 6740, 1987
A;Title: Nucleotide sequence of a full-length cDNA clone encoding preproparathyroid horm
A;Reference number: A26806; MUID:87316938; PMID:3628009
A;Accession: B26806
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-115 <SCH>
A;Cross-references: GB:X05722; GB:Y00409; NID:g1838; PIDN:CAA29193.1; PID:g1839
R;Chu, L.L.H.; Huang, W.Y.; Littledike, E.T.; Hamilton, J.W.; Cohn, D.V.
Biochemistry 14, 3631-3635, 1975
A;Title: Porcine proparathyroid hormone. Identification, biosynthesis, and partial aminc
A;Reference number: A90390; MUID:76018954; PMID:1164500
A;Accession: A90390
A;Molecule type: protein
A;Residues: 26-115 <CHU>
R;Sauer, R.T.; Niall, H.D.; Hogan, M.L.; Keutmann, H.T.; O'Riordan, J.L.H.; Potts Jr., J
Biochemistry 13, 1994-1999, 1974
A;Title: The amino acid sequence of porcine parathyroid hormone.
A;Reference number: A90376; MUID:74253317; PMID:4840833
A;Accession: A90376
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A;Molecule type: protein
A;Residues: 32-109 <SAU>
R;Brewer Jr., H.B.; Fairwell, T.; Rittel, W.; Littledike, T.; Arnaud, C.D.
Am. J. Med. 56, 759-766, 1974
A;Title: Recent studies on the chemistry of human, bovine and porcine parathyroid hor
A;Reference number: A90030; MUID:74173303; PMID:4598526
A;Contents: annotation
C;Superfamily: parathyroid hormone; parathyroid hormone homology
C;Keywords: calcium; hormone; parathyroid gland
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-31/Domain: propeptide #status experimental <PRO>
F;30-64/Domain: parathyroid hormone homology <PTH>
F;32-115/Product: parathyroid hormone #status experimental <MAT>

  Query Match             76.7%;  Score 194;  DB 1;  Length 115;
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  Matches   40;  Conservative    4;  Mismatches    7;  Indels    0;  Gaps    0;

Qy        1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
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Db       65 FVALGASIVHRDGGSQRPRKKEDNVLVESHQKSLGEADKAAVDVLIKAKPQ 115


RESULT 5
I51851
parathyroid hormone - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
C;Accession: I51851
R;Schmelzer, H.
Adv. Gene Technol. 21, 228-229, 1984
A;Title: Nucleotide sequence of cloned cDNA encoding rat prepro parathyroid hormone.
A;Reference number: I51851
A;Accession: I51851
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-105 <RES>
A;Cross-references: GB:M54875; NID:g601932; PIDN:AAA57156.1; PID:g601933
C;Genetics:
A;Gene: PTH
C;Superfamily: parathyroid hormone; parathyroid hormone homology
F;20-54/Domain: parathyroid hormone homology <PTH>

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Qy        1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
            ||:||  :| |:   ||| |||:||||: : ||||| :||||:|| |||||
Db       55 FVSLGVQMAAREGSYQRPTKKEENVLVDGNSKSLGEGDKADVDVLVKAKSQ 105


RESULT 6
A05091
parathyroid hormone precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 16-Jul-1999
C;Accession: A05091; A26806
R;Heinrich, G.; Kronenberg, H.M.; Potts Jr., J.T.; Habener, J.F.
J. Biol. Chem. 259, 3320-3329, 1984
A;Reference number: A05091; MUID:84135846; PMID:6321505
A;Accession: A05091
A;Molecule type: DNA
A;Residues: 1-115 <HEI>
A;Cross-references: GB:K01268; NID:g206483; PIDN:AAA41979.1; PID:g206485
A;Note: the authors translated the codon GAA for residue 87 as Asp
R;Schmelzer, H.J.; Gross, G.; Widera, G.; Mayer, H.
Nucleic Acids Res. 15, 6740, 1987
A;Title: Nucleotide sequence of a full-length cDNA clone encoding preproparathyroid h
A;Reference number: A26806; MUID:87316938; PMID:3628009
A;Accession: A26806
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
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A;Residues: 1-115 <SCH>
A;Cross-references: GB:X05721; GB:Y00409; NID:g56002; PIDN:CAA29192.1; PID:g56003
C;Genetics:
A;Introns: 29/3
C;Superfamily: parathyroid hormone; parathyroid hormone homology
F;30-64/Domain: parathyroid hormone homology <PTH>

  Query Match             63.2%;  Score 160;  DB 2;  Length 115;
  Best Local Similarity   62.7%;  Pred. No. 3.2e-12;
  Matches   32;  Conservative    8;  Mismatches   11;  Indels    0;  Gaps    0;

Qy      1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
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Db     65 FVSLGVQMAAREGSYQRPTKKEENVLVDGNSKSLGEGDKADVDVLVKAKSQ 115


RESULT 7
A34937
parathyroid hormone precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 16-Jul-1999
C;Accession: A34937; I50411
R;Russell, J.; Sherwood, L.M.
Mol. Endocrinol. 3, 325-331, 1989
A;Title: Nucleotide sequence of the DNA complementary to avian (chicken) preproparathyro
A;Reference number: A34937; MUID:89219100; PMID:2710135
A;Accession: A34937
A;Molecule type: mRNA
A;Residues: 1-119 <RUS>
A;Cross-references: GB:M31604; NID:g212767; PIDN:AAA49093.1; PID:g212768
R;Khosla, S.; Demay, M.; Pines, M.; Hurwitz, S.; Potts, J.T.
J. Bone Miner. Res. 3, 689-698, 1988
A;Title: Nucleotide sequence of cloned cDNAs encoding chicken preproparathyroid hormone.
A;Reference number: I50411; MUID:89284968; PMID:3251402
A;Accession: I50411
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-119 <KHO>
A;Cross-references: GB:M36522; NID:g212591; PIDN:AAB02866.1; PID:g212592
C;Superfamily: parathyroid hormone; parathyroid hormone homology
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-31/Domain: propeptide #status predicted <PRO>
F;30-64/Domain: parathyroid hormone homology <PTH>
F;32-119/Product: parathyroid hormone #status predicted <MAT>

  Query Match             27.1%;  Score 68.5;  DB 2;  Length 119;
  Best Local Similarity   38.9%;  Pred. No. 0.39;
  Matches   21;  Conservative    6;  Mismatches   14;  Indels   13;  Gaps    1;

Qy      9 APRDAGSQRPRKKEDNVLVE-------------SHEKSLGEANKADVNVLTKAK 49
          |  || :|||| ||| || |             : :|   : :|| :||| | |
Db     65 ALEDARTQRPRNKEDIVLGEIRNRRLLPEHLRAAVQKKSIDLDKAYMNVLFKTK 118


RESULT 8
H86803
prophage pi3 protein 59 [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C;Accession: H86803
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: H86803
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-283 <STO>
A;Cross-references: GB:AE005176; PID:g12724421; PIDN:AAK05530.1; GSPDB:GN00146
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: pi359
```

```
  Query Match             25.7%;  Score 65;  DB 2;  Length 283;
  Best Local Similarity   36.1%;  Pred. No. 2.6;
  Matches   13;  Conservative    8;  Mismatches   15;  Indels    0;  Gaps    0;

Qy     15 SQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKS 50
          |:  :| : |:|::|  | : : | ||  ||   ||
Db    110 SKESKKSDSNLLIDSQYKEIADENGADSAVLVATKS 145


RESULT 9
A71407
probable Ste20-like kinase - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
A;Variety: columbia
C;Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 16-Dec-1998
C;Accession: A71407
R;Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; D
 P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenegger, T.; Pohl, T.M.; Terryn, N.; G
avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B
Nature 391, 485-488, 1998
A;Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomen
erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.;
C.; Chalwatzis, N.
A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis t
A;Reference number: A71400; MUID:98121113; PMID:9461215
A;Accession: A71407
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-487 <BEV>
A;Cross-references: GB:Z97336; NID:g2244788; PID:e326893; PID:g2244804
C;Genetics:
A;Map position: 4COP9-4G3845
C;Superfamily: protein kinase homology
F;13-293/Domain: protein kinase homology <KIN>

  Query Match             25.1%;  Score 63.5;  DB 2;  Length 487;
  Best Local Similarity   30.2%;  Pred. No. 7.1;
  Matches   13;  Conservative   12;  Mismatches   11;  Indels    7;  Gaps    1;

Qy      9 APRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
          :||:    : :|::||| :  :|  || :|:       :||:|
Db    374 SPREEDQSKDKKEDDNVTITGYELGLGLSNE-------EAKNQ 409


RESULT 10
I38055
myosin heavy chain, perinatal skeletal muscle - human
N;Contains: myosin ATPase (EC 3.6.4.1)
C;Species: Homo sapiens (man)
C;Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 19-Apr-2002
C;Accession: I38055; JH0154; S12459; S09332; A30220; S49478
R;Jullian, E.H.; Kelly, A.M.; Pompidou, A.J.; Hoffman, R.; Schiaffino, S.; Stedman, H
Eur. J. Biochem. 230, 1001-1006, 1995
A;Title: Characterization of a human perinatal myosin heavy-chain transcript.
A;Reference number: I38055; MUID:95324556; PMID:7601129
A;Accession: I38055
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1937 <RES>
A;Cross-references: EMBL:Z38133; NID:g558668; PIDN:CAA86293.1; PID:g558669
R;Karsch-Mizrachi, I.; Feghali, R.; Shows, T.B.; Leinwand, L.A.
Gene 89, 289-294, 1990
A;Title: Generation of a full-length human perinatal myosin heavy-chain-encoding cDNA
A;Reference number: JH0154; MUID:90323631; PMID:2373371
A;Accession: JH0154
A;Molecule type: mRNA
A;Residues: 1-14,'A',16-859 <KAR>
A;Cross-references: GB:Y00821
A;Experimental source: skeletal muscle
R;Bober, E.
submitted to the EMBL Data Library, January 1989
A;Reference number: S12458
A;Accession: S12459
```

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A;Molecule type: mRNA
A;Residues: 502-1071,'N',1073-1250,'DGG',1253-1376,'NT',1379-1913,'D',1915-1937 <BOB>
A;Cross-references: EMBL:X51592; NID:g29465; PIDN:CAA35941.1; PID:g29466
A;Experimental source: clone gtMHC-F
R;Bober, E.; Buchberger-Seidl, A.; Braun, T.; Singh, S.; Goedde, H.W.; Arnold, H.H.
Eur. J. Biochem. 189, 55-65, 1990
A;Title: Identification of three developmentally controlled isoforms of human myosin hea
A;Reference number: S09331; MUID:90235862; PMID:1691980
A;Accession: S09332
A;Molecule type: mRNA
A;Residues: 502-547,'X',549-617,'X',619-687,'X',689-757,'X',759-827,'X',829-897,'X',899-
-1376,'NT',1379-1386,'X',1388-1456,'X',1458-1526,'X',1528-1596,'X',1598-1666,'X',1668-17
A;Cross-references: EMBL:X51592
R;Feghali, R.; Leinwand, L.A.
J. Cell Biol. 108, 1791-1797, 1989
A;Title: Molecular genetic characterization of a developmentally regulated human perinat
A;Reference number: A30220; MUID:89234168; PMID:2715179
A;Accession: A30220
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 860-969,'Q',971-1246,'H',1248-1260,'G',1262-1296,'Q',1298-1503,'AH',1506-184
A;Cross-references: GB:Y00821; NID:g34863; PIDN:CAA68757.1; PID:g34864
C;Genetics:
A;Gene: GDB:MYH8
A;Cross-references: GDB:125267; OMIM:160741
A;Map position: 17pter-17p12
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: actin binding; ATP; coiled coil; hydrolase; muscle contraction; nucleotide b
F;91-769/Domain: myosin motor domain homology <MMOT>
F;181-188/Region: nucleotide-binding motif A (P-loop)
F;551-588/Region: actin binding #status predicted
F;658-680/Region: actin binding #status predicted
F;842-1282/Region: S2 #status predicted
F;698,708/Active site: Cys #status predicted

  Query Match             24.9%;  Score 63;  DB 2;  Length 1937;
  Best Local Similarity   42.4%;  Pred. No. 35;
  Matches   14;  Conservative    9;  Mismatches    8;  Indels    2;  Gaps    1;

Qy      21 KEDNVLVESHEKSLG--EANKADVNVLTKAKSQ 51
           ||   | |:|:::|   :| :  ||:|||||::
Db     997 KEKKALQETHQQTLDDLQAEEDKVNILTKAKTK 1029


RESULT 11
A64028
hypothetical protein HI1405 - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999
C;Accession: A64028
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J
, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: A64028
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-366 <TIGR>
A;Cross-references: GB:U32820; GB:L42023; NID:g1574231; PIDN:AAC23055.1; PID:g1574243; T

  Query Match             24.3%;  Score 61.5;  DB 2;  Length 366;
  Best Local Similarity   35.6%;  Pred. No. 9.1;
  Matches   16;  Conservative   10;  Mismatches   18;  Indels    1;  Gaps    1;

Qy       7 PLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
           |  |::  |:   ||||:|  |  |||| :|   ::  |  |:::
Db     222 PTKPKEKKSEPENKKEDDVEKEELEKSL-KAKDEEIQQLKDAQAK 265


RESULT 12
```

```
G89813
DNA polymerase III gamma and tau subunits [imported] - Staphylococcus aureus (strain
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: G89813
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; O
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K
 C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: G89813
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-565 <KUR>
A;Cross-references: GB:BA000018; PID:g13700368; PIDN:BAB41666.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A;Gene: dnaX
C;Superfamily: DNA-directed DNA polymerase III gamma chain

  Query Match             24.1%;  Score 61;  DB 2;  Length 565;
  Best Local Similarity   31.9%;  Pred. No. 17;
  Matches   15;  Conservative   11;  Mismatches   17;  Indels    4;  Gaps    1;

Qy       3 ALGAPLAPRDAGSQRP----RKKEDNVLVESHEKSLGEANKADVNVL 45
           | |  :||    |::|    :| ::   ::   | | :|||||: :|
Db     391 AQGVSVAPAQKSSKKPARGIQKSKNAFSMQQIAKVLDKANKADIKLL 437


RESULT 13
T44010
virion protein [imported] - human herpesvirus 6
C;Species: human herpesvirus 6
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C;Accession: T44010; T44197
R;Isegawa, Y.; Mukai, T.; Nakano, K.; Kagawa, M.; Chen, J.; Mori, Y.; Sunagawa, T.; K
J. Virol. 73, 8053-8063, 1999
A;Title: Comparison of the complete DNA sequences of human herpesvirus 6 variants A a
A;Reference number: Z22732; MUID:99412319; PMID:10482554
A;Accession: T44010
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-555 <ISE>
A;Cross-references: EMBL:AB021506; NID:g4995977; PIDN:BAA78271.1; PID:g4996038
A;Experimental source: strain HST; pop. variant B
R;Dominguez, G.; Dambaugh, T.R.; Stamey, F.R.; Dewhurst, S.; Inoue, N.; Pellett, P.E.
J. Virol. 73, 8040-8052, 1999
A;Title: Human herpesvirus 6B genome sequence: coding content and comparison with hum
A;Reference number: Z22734; MUID:99412318; PMID:10482553
A;Accession: T44197
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-555 <DOM>
A;Cross-references: EMBL:AF157706; PIDN:AAB06348.1
A;Experimental source: strain Z29; variant B
C;Genetics:
A;Gene: U50
C;Superfamily: varicella-zoster virus gene 34 protein

  Query Match             23.9%;  Score 60.5;  DB 2;  Length 555;
  Best Local Similarity   42.5%;  Pred. No. 19;
  Matches   17;  Conservative    8;  Mismatches   10;  Indels    5;  Gaps    2;

Qy      16 QRPRKKEDNVLVESHEKSLGEA----NKADVNVLTKAKSQ 51
           ||  :|: :||  || |:: :|    |  :||| ||| :|
Db      67 QRKMQKDSDVL-NSHLKAIEDALLFTNDGEVNVETKADTQ 105


RESULT 14
A02985
myosin heavy chain, skeletal muscle - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
```

```
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 13-Feb-1998
C;Accession: A02985
R;Capony, J.P.; Elzinga, M.
Biophys. J. 33, 148a, 1981
A;Reference number: A02985
A;Accession: A02985
A;Molecule type: protein
A;Residues: 1-258 <CAP>
A;Note: this fragment is from the heavy meromyosin subfragment-2
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: actin binding; ATP; coiled coil; muscle; skeletal muscle

  Query Match             23.7%;  Score 60;  DB 2;  Length 258;
  Best Local Similarity   42.4%;  Pred. No. 9.6;
  Matches   14;  Conservative    8;  Mismatches    9;  Indels    2;  Gaps    1;

Qy      21 KEDNVLVESHEKSLG--EANKADVNVLTKAKSQ 51
           ||   | |:|:::|   :| :  || |||||::
Db     152 KEKKALQEAHQQTLDDLQAEEDKVNTLTKAKTK 184


RESULT 15
S24348
myosin heavy chain, embryonic and adult skeletal muscle (clone Cemb2) - chicken (fragmen
C;Species: Gallus gallus (chicken)
C;Date: 03-Feb-1994 #sequence_revision 06-Sep-1996 #text_change 13-Feb-1998
C;Accession: S24348
R;Moore, L.A.; Arrizubieta, M.J.; Tidyman, W.E.; Herman, L.A.; Bandman, E.
J. Mol. Biol. 225, 1143-1151, 1992
A;Title: Analysis of the chicken fast myosin heavy chain family. Localization of isoforn
A;Reference number: S24348; MUID:92309413; PMID:1377278
A;Accession: S24348
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-955 <MOO>
A;Cross-references: EMBL:M74085
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: ATP; coiled coil; muscle contraction; skeletal muscle; thick filament

  Query Match             23.7%;  Score 60;  DB 2;  Length 955;
  Best Local Similarity   42.4%;  Pred. No. 38;
  Matches   14;  Conservative    8;  Mismatches    9;  Indels    2;  Gaps    1;

Qy      21 KEDNVLVESHEKSLG--EANKADVNVLTKAKSQ 51
           ||   | |:|:::|   :| :  || |||||::
Db      13 KEKKALQEAHQQTLDDLQAEEDKVNTLTKAKTK 45


Search completed: March 13, 2003, 15:02:26
Job time : 10.8955 secs
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                        GenCore version 5.1.4_p5_4578
               Copyright (c) 1993 - 2003  Compugen Ltd.

OM protein - protein search, using sw model

Run on:         March 13, 2003, 14:52:59 ; Search time 5.70896 Seconds
                                           (without alignments)
                                           370.522 Million cell updates/sec

Title:          US-09-636-530-3
Perfect score:  253
Sequence:       1 FVALGAPLAPRDAGSQRPRK..........KSLGEANKADVNVLTKAKSQ 51

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters:      112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       SwissProt_40:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                 SUMMARIES
                  %
Result          Query
  No.   Score   Match Length DB  ID                      Description
-----------------------------------------------------------------------
    1     248    98.0    115  1  PTHY_HUMAN              P01270 homo sapien
    2     241    95.3    115  1  PTH_MACFA               Q9xt35 macaca fasc
    3     206    81.4    115  1  PTHY_CANFA              P52212 canis famil
    4     199    78.7    115  1  PTHY_BOVIN              P01268 bos taurus
    5     194    76.7    115  1  PTHY_PIG                P01269 sus scrofa
    6     160    63.2    115  1  PTHY_RAT                P04089 rattus norv
    7    68.5    27.1    119  1  PTHY_CHICK              P15743 gallus gall
    8      63    24.9   1937  1  MYH8_HUMAN              P13535 homo sapien
    9    61.5    24.3    366  1  YE05_HAEIN              P44180 haemophilus
   10    60.5    23.9    555  1  UL25_HSV6Z              P52537 human herpe
   11      60    23.7   1084  1  MYSS_RABIT              P02562 oryctolagus
   12      60    23.7   1935  1  MYSS_CYPCA              Q90339 cyprinus ca
   13      60    23.7   1938  1  MYH4_RABIT              Q28641 oryctolagus
   14      60    23.7   1940  1  MYH3_CHICK              P02565 gallus gall
   15    58.5    23.1    527  1  ATRX_RAT                P70486 rattus norv
   16      58    22.9    465  1  MYH6_RABIT              P04460 oryctolagus
   17      58    22.9    599  1  KLC2_MOUSE              O88448 mus musculu
   18      58    22.9   1935  1  MYH7_HUMAN              P12883 homo sapien
   19      58    22.9   1935  1  MYH7_PIG                P79293 sus scrofa
   20      58    22.9   1935  1  MYH7_RAT                P02564 rattus norv
   21      58    22.9   1939  1  MYH1_HUMAN              P12882 homo sapien
   22      58    22.9   1941  1  MYH2_HUMAN              Q9ukx2 homo sapien
   23    57.5    22.7    378  1  UL25_HSV6G              P52536 human herpe
   24    57.5    22.7    555  1  UL25_HSV6U              P52387 human herpe
   25      57    22.5   1939  1  MYH4_HUMAN              Q9y623 homo sapien
   26      56    22.1   1938  1  MYSS_CHICK              P13538 gallus gall
   27    55.5    21.9   2426  1  SON_HUMAN               P18583 homo sapien
   28      55    21.7    831  1  NFH_RAT                 P16884 rattus norv
   29      55    21.7   1154  1  KDGD_MESAU              Q64398 mesocricetu
   30      55    21.7   1157  1  YE56_CAEEL              P90747 caenorhabdi
   31      55    21.7   1518  1  KKK1_YEAST              P34244 saccharomyc
   32      55    21.7   1934  1  MYH7_MESAU              P13540 mesocricetu
   33      55    21.7   1938  1  MYH6_MOUSE              Q02566 mus musculu
   34      55    21.7   1938  1  MYH6_RAT                P02563 rattus norv
   35      55    21.7   1939  1  MYH6_MESAU              P13539 mesocricetu
   36    54.5    21.5    587  1  GCDA_ACIFE              Q06700 acidaminoco
   37      54    21.3     67  1  HARB_PYRAB              Q9v1f5 pyrococcus
   38      54    21.3     67  1  HARB_PYRHO              O74092 pyrococcus
   39      54    21.3    325  1  TDG_SCHPO               O59825 schizosacch
   40      54    21.3    622  1  KLC2_HUMAN              Q9h0b6 homo sapien
   41      54    21.3    736  1  MYH7_RABIT              P04461 oryctolagus
   42      54    21.3    960  1  VP41_LYCES              P93231 lycopersico
   43      54    21.3    983  1  PTPN_RAT                Q63259 rattus norv
   44      54    21.3   1033  1  Y328_MYCPN              P75310 mycoplasma
   45    53.5    21.1    626  1  CEIB_ECOLI              P04479 escherichia

                                  ALIGNMENTS

RESULT 1
PTHY_HUMAN
ID   PTHY_HUMAN     STANDARD;      PRT;   115 AA.
AC   P01270;
DT   21-JUL-1986 (Rel. 01, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Parathyroid hormone precursor (Parathyrin) (PTH) (Parathormone).
GN   PTH.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=82150870; PubMed=6950381;
RA   Hendy G.N., Kronenberg H.M., Potts J.T. Jr., Rich A.;
RT   "Nucleotide sequence of cloned cDNAs encoding human preproparathyroid
RT   hormone.";
RL   Proc. Natl. Acad. Sci. U.S.A. 78:7365-7369(1981).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83169834; PubMed=6220408;
RA   Vasicek T.J., McCevitt B.E., Freeman M.W., Fennick B.J.,
RA   Hendy G.N., Potts J.T. Jr., Rich A., Kronenberg H.M.;
RT   "Nucleotide sequence of the human parathyroid hormone gene.";
RL   Proc. Natl. Acad. Sci. U.S.A. 80:2127-2131(1983).
RN   [3]
RP   SEQUENCE OF 26-37.
RX   MEDLINE=74174967; PubMed=4833516;
RA   Jacobs J.W., Kemper B., Niall H.D., Habener J.F., Potts J.T. Jr.;
RT   "Structural analysis of human proparathyroid hormone by a new
RT   microsequencing approach.";
RL   Nature 249:155-157(1974).
RN   [4]
RP   SEQUENCE OF 32-68.
RX   MEDLINE=74111656; PubMed=4521809;
RA   Niall H.D., Sauer R.T., Jacobs J.W., Keutmann H.T., Segre G.V.,
RA   O'Riordan J.L.H., Aurbach G.D., Potts J.T. Jr.;
RT   "The amino-acid sequence of the amino-terminal 37 residues of human
RT   parathyroid hormone.";
RL   Proc. Natl. Acad. Sci. U.S.A. 71:384-388(1974).
RN   [5]
RP   SEQUENCE OF 61-83 AND 84-115.
RX   MEDLINE=79082855; PubMed=728431;
RA   Keutmann H.T., Sauer M.M., Hendy G.N., O'Riordan J.L.H.,
RA   Potts J.T. Jr.;
RT   "Complete amino acid sequence of human parathyroid hormone.";
RL   Biochemistry 17:5723-5729(1978).
RN   [6]
RP   SEQUENCE OF 75-100.
RA   Keutmann H.T., Niall H.D., Jacobs J.W., Barling P.M., Hendy G.N.,
RA   O'Riordan J.L.H., Potts J.T. Jr.;
RL   (In) Talmadge R.V., Owen M., Parsons J.A. (eds.);
RL   Calcium-regulating hormones, pp.9-14, Excerpta Medica Foundation,
RL   Amsterdam (1975).
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RN   [7]
RP   REVISIONS.
RX   MEDLINE=75146516; PubMed=1125201;
RA   Keutmann H.T., Niall H.D., O'Riordan J.L.H., Potts J.T. Jr.;
RT   "A reinvestigation of the amino-terminal sequence of human
RT   parathyroid hormone.";
RL   Biochemistry 14:1842-1847(1975).
RN   [8]
RP   SYNTHESIS OF 32-65.
RX   MEDLINE=75059220; PubMed=4474131;
RA   Tregear G.W., van Rietschoten J., Green E., Niall H.D.,
RA   Keutmann H.T., Parsons J.A., O'Riordan J.L.H., Potts J.T. Jr.;
RT   "Solid-phase synthesis of the biologically active N-terminal 1-34
RT   peptide of human parathyroid hormone.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 355:415-421(1974).
RN   [9]
RP   SYNTHESIS OF 32-65.
RX   MEDLINE=73227467; PubMed=4721748;
RA   Andreatta R.H., Hartmann A., Joehl A., Kamber B., Maier R.,
RA   Riniker B., Rittel W., Sieber P.;
RT   "Synthesis of sequence 1-34 of human parathyroid hormone.";
RL   Helv. Chim. Acta 56:470-473(1973).
RN   [10]
RP   STRUCTURE BY NMR OF 32-65.
RX   MEDLINE=91299748; PubMed=2069952;
RA   Klaus W., Dieckmann T., Wray V., Schomburg D., Wingender E., Mayer H.;
RT   "Investigation of the solution structure of the human parathyroid
RT   hormone fragment (1-34) by 1H NMR spectroscopy, distance geometry,
RT   and molecular dynamics calculations.";
RL   Biochemistry 30:6936-6942(1991).
RN   [11]
RP   STRUCTURE BY NMR OF 32-65.
RX   MEDLINE=93345518; PubMed=8344299;
RA   Barden J.A., Cuthbertson R.M.;
RT   "Stabilized NMR structure of human parathyroid hormone(1-34).";
RL   Eur. J. Biochem. 215:315-321(1993).
RN   [12]
RP   STRUCTURE BY NMR OF 32-68.
RX   MEDLINE=95318084; PubMed=7797503;
RA   Marx U.C., Austermann S., Bayer P., Adermann K., Ejchart A.,
RA   Sticht H., Walter S., Schmid F.-X., Jaenicke R., Forssmann W.-G.,
RA   Roesch P.;
RT   "Structure of human parathyroid hormone 1-37 in solution.";
RL   J. Biol. Chem. 270:15194-15202(1995).
RN   [13]
RP   STRUCTURE BY NMR OF 32-70.
RX   MEDLINE=20090619; PubMed=10623601;
RA   Marx U.C., Adermann K., Bayer P., Forssmann W.-G., Rosch P.;
RT   "Solution structures of human parathyroid hormone fragments
RT   hPTH(1-34) and hPTH(1-39) and bovine parathyroid hormone fragment
RT   bPTH(1-37).";
RL   Biochem. Biophys. Res. Commun. 267:213-220(2000).
RN   [14]
RP   VARIANT ARG-18.
RX   MEDLINE=91009811; PubMed=2212001;
RA   Arnold A., Horst S.A., Gardella T.J., Baba H., Levine M.A.,
RA   Kronenberg H.M.;
RT   "Mutation of the signal peptide-encoding region of the
RT   preproparathyroid hormone gene in familial isolated
RT   hypoparathyroidism.";
RL   J. Clin. Invest. 86:1084-1087(1990).
CC   -!- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC       BONE AND PREVENTING THEIR RENAL EXCRETION.
CC   -!- DISEASE: DEFECTS IN PTH ARE A CAUSE OF FAMILIAL ISOLATED
CC       HYPOPARATHYROIDISM (FIH).
CC   -!- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; J00301; AAA60215.1; -.
DR   EMBL; V00597; CAA23843.1; -.
DR   EMBL; A29146; CAA01956.1; -.
DR   PIR; A01536; PTHU.
DR   PIR; A19339; A19339.
DR   PDB; 1HPH; 10-JUL-95.
DR   PDB; 1HTH; 15-OCT-97.
DR   PDB; 1ZWA; 12-MAR-97.
DR   PDB; 1ZWB; 12-MAR-97.
DR   PDB; 1ZWD; 12-MAR-97.
DR   PDB; 1ZWE; 12-MAR-97.
DR   PDB; 1ZWF; 16-JUN-97.
DR   PDB; 1ZWG; 16-JUN-97.
DR   PDB; 1BWX; 14-JAN-00.
DR   PDB; 1HPY; 14-JAN-00.
DR   Genew; HGNC:9606; PTH.
DR   MIM; 146200; -.
DR   MIM; 168450; -.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   Pfam; PF01279; Parathyroid; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   SMART; SM00087; PTH; 1.
DR   PROSITE; PS00335; PARATHYROID; 1.
KW   Hormone; Signal; Disease mutation; 3D-structure.
FT   SIGNAL        1     25
FT   PROPEP       26     31
FT   CHAIN        32    115       PARATHYROID HORMONE.
FT   VARIANT      18     18       C -> R (IN FIH; LEADS TO INEFFICIENT
FT                                PROCESSING OF THE PRECURSOR).
FT                                /FTId=VAR_006047.
FT   CONFLICT    107    107       N -> D (IN REF. 5).
SQ   SEQUENCE   115 AA;  12861 MW;  849015736A6E5597 CRC64;

  Query Match             98.0%;  Score 248;  DB 1;  Length 115;
  Best Local Similarity   98.0%;  Pred. No. 1.2e-23;
  Matches   50;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
              |||||||||||||||||||||||||||||||||||||:|||||||||||||
Db         65 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEADKADVNVLTKAKSQ 115


RESULT 2
PTH_MACFA
ID   PTH_MACFA      STANDARD;      PRT;   115 AA.
AC   Q9XT35;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Parathyroid hormone precursor (Parathyrin) (PTH).
GN   PTH.
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Malaivijitnond S., Takenaka O.;
RT   "Nucleotide sequences of parathyroid gene in five species of macaque
RT   of Thailand.";
RL   J. Sci. Res. Chulalongkorn Univ. 23:135-142(1998).
CC   -!- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC       BONE AND PREVENTING THEIR RENAL EXCRETION.
CC   -!- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
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CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; AF130257; AAD42777.1; -.
DR   HSSP; P01270; 1HPY.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   Pfam; PF01279; Parathyroid; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   SMART; SM00087; PTH; 1.
DR   PROSITE; PS00335; PARATHYROID; 1.
KW   Hormone; Signal.
FT   SIGNAL        1     25       BY SIMILARITY.
FT   PROPEP       26     31       BY SIMILARITY.
FT   CHAIN        32    115       PARATHYROID HORMONE.
SQ   SEQUENCE   115 AA;  12890 MW;  8C2500EF24BE5597 CRC64;

  Query Match             95.3%;  Score 241;  DB 1;  Length 115;
  Best Local Similarity   92.2%;  Pred. No. 8.4e-23;
  Matches   47;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
          |:||||||||||||||||||||||:||||||||||||:||||:||||||||
Db     65 FIALGAPLAPRDAGSQRPRKKEDNILVESHEKSLGEADKADVDVLTKAKSQ 115


RESULT 3
PTHY_CANFA
ID   PTHY_CANFA     STANDARD;      PRT;   115 AA.
AC   P52212;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   Parathyroid hormone precursor (Parathyrin) (PTH).
GN   PTH.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Parathyroid;
RX   MEDLINE=95369696; PubMed=7642102;
RA   Rosol T.J., Steinmeyer C.L., McCauley L.K., Groene A.,
RA   DeWille J.W., Capen C.C.;
RT   "Sequences of the cDNAs encoding canine parathyroid hormone-related
RT   protein and parathyroid hormone.";
RL   Gene 160:241-243(1995).
CC   -!- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC       BONE AND PREVENTING THEIR RENAL EXCRETION.
CC   -!- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; U15662; AAA82584.1; -.
DR   HSSP; P01268; 1ZWC.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   Pfam; PF01279; Parathyroid; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   SMART; SM00087; PTH; 1.
DR   PROSITE; PS00335; PARATHYROID; 1.
KW   Hormone; Signal.
FT   SIGNAL        1     25       BY SIMILARITY.
FT   PROPEP       26     31       BY SIMILARITY.
FT   CHAIN        32    115       PARATHYROID HORMONE.
SQ   SEQUENCE   115 AA;  12957 MW;  FC38F77F1C8CFE56 CRC64;

  Query Match             81.4%;  Score 206;  DB 1;  Length 115;
  Best Local Similarity   82.4%;  Pred. No. 1.6e-18;
  Matches   42;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
          |||||||:| ||  |||| ||||||||||::||||||:||||:||||||||
Db     65 FVALGAPIAHRDGSSQRPLKKEDNVLVESYQKSLGEADKADVDVLTKAKSQ 115


RESULT 4
PTHY_BOVIN
ID   PTHY_BOVIN     STANDARD;      PRT;   115 AA.
AC   P01268;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Parathyroid hormone precursor (Parathyrin) (PTH).
GN   PTH.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=80056617; PubMed=388425;
RA   Kronenberg H.M., McDevitt B.E., Majzoub J.A., Nathans J., Sharp P.A.,
RA   Potts J.T. Jr., Rich A.;
RT   "Cloning and nucleotide sequence of DNA coding for bovine
RT   preproparathyroid hormone.";
RL   Proc. Natl. Acad. Sci. U.S.A. 76:4981-4985(1979).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=82037785; PubMed=6170060;
RA   Weaver C.A., Gordon D.F., Kemper B.;
RT   "Introduction by molecular cloning of artifactual inverted sequences
RT   at the 5' terminus of the sense strand of bovine parathyroid hormone
RT   cDNA.";
RL   Proc. Natl. Acad. Sci. U.S.A. 78:4073-4077(1981).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83105964; PubMed=6185374;
RA   Weaver C.A., Gordon D.F., Kemper B.;
RT   "Nucleotide sequence of bovine parathyroid hormone messenger RNA.";
RL   Mol. Cell. Endocrinol. 28:411-424(1982).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=84262483; PubMed=6086460;
RA   Weaver C.A., Gordon D.F., Kissil M.S., Mead D.A., Kemper B.;
RT   "Isolation and complete nucleotide sequence of the gene for bovine
RT   parathyroid hormone.";
RL   Gene 28:319-329(1984).
RN   [5]
RP   SEQUENCE OF 26-115.
RX   MEDLINE=74142666; PubMed=4522780;
RA   Hamilton J.W., Niall H.D., Jacobs J.W., Keutmann H.T., Potts J.T. Jr.,
RA   Cohn D.V.;
RT   "The N-terminal amino-acid sequence of bovine proparathyroid
RT   hormone.";
RL   Proc. Natl. Acad. Sci. U.S.A. 71:653-656(1974).
RN   [6]
RP   SEQUENCE OF 32-115.
RX   MEDLINE=71076162; PubMed=5531031;
RA   Niall H.D., Keutmann H.T., Sauer R., Hogan M.L., Dawson B.F.,
RA   Aurbach G.D., Potts J.T. Jr.;
RT   "The amino acid sequence of bovine parathyroid hormone I.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 351:1586-1588(1970).
RN   [7]
RP   SEQUENCE OF 32-115.
RX   MEDLINE=71063634; PubMed=5275384;
RA   Brewer H.B. Jr., Ronan R.;
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RT   "Bovine parathyroid hormone: amino acid sequence.";
RL   Proc. Natl. Acad. Sci. U.S.A. 67:1862-1869(1970).
RN   [8]
RP   SYNTHESIS OF 32-65.
RX   MEDLINE=71091588; PubMed=4322265;
RA   Potts J.T. Jr., Tregear G.W., Keutmann H.T., Niall H.D., Sauer R.,
RA   Deftos L.J., Dawson B.F., Hogan M.L., Aurbach G.D.;
RT   "Synthesis of a biologically active N-terminal tetratriacontapeptide
RT   of parathyroid hormone.";
RL   Proc. Natl. Acad. Sci. U.S.A. 68:63-67(1971).
RN   [9]
RP   STRUCTURE BY NMR OF 32-68.
RX   MEDLINE=20090619; PubMed=10623601;
RA   Marx U.C., Adermann K., Bayer P., Forssmann W.-G., Rosch P.;
RT   "Solution structures of human parathyroid hormone fragments
RT   hPTH(1-34) and hPTH(1-39) and bovine parathyroid hormone fragment
RT   bPTH(1-37).";
RL   Biochem. Biophys. Res. Commun. 267:213-220(2000).
CC   -!- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC       BONE AND PREVENTING THEIR RENAL EXCRETION.
CC   -!- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
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CC   --------------------------------------------------------------------------
DR   EMBL; V00106; CAA23439.1; -.
DR   EMBL; J00024; AAA30747.1; -.
DR   EMBL; K01938; AAA30749.1; -.
DR   EMBL; M25082; AAA30748.1; -.
DR   PIR; A01534; PTBO.
DR   PIR; A24949; A24949.
DR   PDB; 1ZWC; 12-MAR-97.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   Pfam; PF01279; Parathyroid; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   SMART; SM00087; PTH; 1.
DR   PROSITE; PS00335; PARATHYROID; 1.
KW   Hormone; Signal; 3D-structure.
FT   SIGNAL        1     25
FT   PROPEP       26     31
FT   CHAIN        32    115       PARATHYROID HORMONE.
FT   CONFLICT    106    106       V -> G (IN REF. 4).
SQ   SEQUENCE   115 AA;  12980 MW;  2ED246B348880710 CRC64;

  Query Match             78.7%;  Score 199;  DB 1;  Length 115;
  Best Local Similarity   80.4%;  Pred. No. 1.2e-17;
  Matches   41;  Conservative    4;  Mismatches    6;  Indels    0;  Gaps    0;

Qy        1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
            |||||| :| ||  ||||||||||||||||:||||||:||||:|| ||| |
Db       65 FVALGASIAYRDGSSQRPRKKEDNVLVESHQKSLGEADKADVDVLIKAKPQ 115


RESULT 5
PTHY_PIG
ID   PTHY_PIG       STANDARD;      PRT;   115 AA.
AC   P01269;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   Parathyroid hormone precursor (Parathyrin) (PTH).
GN   PTH.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
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RP   SEQUENCE FROM N.A.
RX   MEDLINE=87316938; PubMed=3628009;
RA   Schmelzer H.-J., Gross G., Widera G., Mayer H.;
RT   "Nucleotide sequence of a full-length cDNA clone encoding
RT   preproparathyroid hormone from pig and rat.";
RL   Nucleic Acids Res. 15:6740-6740(1987).
RN   [2]
RP   SEQUENCE OF 26-115.
RX   MEDLINE=76018954; PubMed=1164500;
RA   Chu L.L.H., Huang W.-Y., Littledike E.T., Hamilton J.W., Cohn D.V.;
RT   "Porcine proparathyroid hormone. Identification, biosynthesis, and
RT   partial amino acid sequence.";
RL   Biochemistry 14:3631-3635(1975).
RN   [3]
RP   SEQUENCE OF 32-115.
RX   MEDLINE=74253317; PubMed=4840833;
RA   Sauer R.T., Niall H.D., Hogan M.L., Keutmann H.T., O'Riordan J.L.H.,
RA   Potts J.T. Jr.;
RT   "The amino acid sequence of porcine parathyroid hormone.";
RL   Biochemistry 13:1994-1999(1974).
CC   -!- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC       BONE AND PREVENTING THEIR RENAL EXCRETION.
CC   -!- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
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CC   --------------------------------------------------------------------------
DR   EMBL; X05722; CAA29193.1; -.
DR   PIR; A01535; PTPG.
DR   PIR; B26806; B26806.
DR   HSSP; P01270; 1BWX.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   Pfam; PF01279; Parathyroid; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   SMART; SM00087; PTH; 1.
DR   PROSITE; PS00335; PARATHYROID; 1.
KW   Hormone; Signal.
FT   SIGNAL        1     25
FT   PROPEP       26     31
FT   CHAIN        32    115       PARATHYROID HORMONE.
SQ   SEQUENCE   115 AA;  12852 MW;  9FE8BCDE614BAC16 CRC64;

  Query Match             76.7%;  Score 194;  DB 1;  Length 115;
  Best Local Similarity   78.4%;  Pred. No. 4.9e-17;
  Matches   40;  Conservative    4;  Mismatches    7;  Indels    0;  Gaps    0;

Qy        1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
            |||||| :  || |||||||||||||||||:||||||:|| |:|| ||| |
Db       65 FVALGASIVHRDGGSQRPRKKEDNVLVESHQKSLGEADKAAVDVLIKAKPQ 115


RESULT 6
PTHY_RAT
ID   PTHY_RAT       STANDARD;      PRT;   115 AA.
AC   P04089; Q63473;
DT   01-NOV-1986 (Rel. 03, Created)
DT   01-NOV-1986 (Rel. 03, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Parathyroid hormone precursor (Parathyrin) (PTH).
GN   PTH.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=84135846; PubMed=6321505;
```

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RA   Heinrich G., Kronenberg H.M., Potts J.T. Jr., Habener J.F.;
RT   "Gene encoding parathyroid hormone. Nucleotide sequence of the rat
RT   gene and deduced amino acid sequence of rat preproparathyroid
RT   hormone.";
RL   J. Biol. Chem. 259:3320-3329(1984).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87316938; PubMed=3628009;
RA   Schmelzer H.-J., Gross G., Widera G., Mayer H.;
RT   "Nucleotide sequence of a full-length cDNA clone encoding
RT   preproparathyroid hormone from pig and rat.";
RL   Nucleic Acids Res. 15:6740-6740(1987).
RN   [3]
RP   SEQUENCE OF 10-115 FROM N.A.
RC   TISSUE=Parathyroid;
RA   Schmelzer H.J., Gross G., Mayer H.;
RT   "Nucleotide sequence of cloned cDNA encoding rat prepro parathyroid
RT   hormone.";
RL   Adv. Gene Technol. 21:228-229(1984).
RN   [4]
RP   SEQUENCE OF 32-115 FROM N.A.
RC   STRAIN=Sprague-Dawley; TISSUE=Brain, Parathyroid, and Liver;
RX   MEDLINE=96079910; PubMed=7588314;
RA   Nutley M.T., Parimi S.A., Harvey S.;
RT   "Sequence analysis of hypothalamic parathyroid hormone messenger
RT   ribonucleic acid.";
RL   Endocrinology 136:5600-5607(1995).
CC   -!- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC       BONE AND PREVENTING THEIR RENAL EXCRETION.
CC   -!- TISSUE SPECIFICITY: HYPOTHALAMUS AND PARATHYROID GLAND.
CC   -!- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
CC   --------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; K01268; AAA41979.1; -.
DR   EMBL; X05721; CAA29192.1; -.
DR   EMBL; M54875; AAA57156.1; -.
DR   EMBL; S80127; -; NOT_ANNOTATED_CDS.
DR   PIR; A05091; A05091.
DR   PIR; A26806; A26806.
DR   HSSP; P01270; 1ZWB.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   Pfam; PF01279; Parathyroid; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   SMART; SM00087; PTH; 1.
DR   PROSITE; PS00335; PARATHYROID; 1.
KW   Hormone; Signal.
FT   SIGNAL        1     25
FT   PROPEP       26     31
FT   CHAIN        32    115       PARATHYROID HORMONE.
FT   CONFLICT     18     18       C -> Y (IN REF. 3).
FT   CONFLICT     23     23       A -> T (IN REF. 3).
FT   CONFLICT     33     33       V -> I (IN REF. 3).
FT   CONFLICT     62     62       V -> G (IN REF. 3).
SQ   SEQUENCE   115 AA;  12722 MW;  7B434CFCA528B230 CRC64;

  Query Match             63.2%;  Score 160;  DB 1;  Length 115;
  Best Local Similarity   62.7%;  Pred. No. 7.2e-13;
  Matches   32;  Conservative    8;  Mismatches   11;  Indels    0;  Gaps    0;

Qy      1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
          ||:||  :| |:   ||| |||:||||: : ||||| :||||:|| |||||
Db     65 FVSLGVQMAAREGSYQRPTKKEENVLVDGNSKSLGEGDKADVDVLVKAKSQ 115

RESULT 7
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```
PTHY_CHICK
ID   PTHY_CHICK     STANDARD;      PRT;   119 AA.
AC   P15743;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-APR-1990 (Rel. 14, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   Parathyroid hormone precursor (PTH).
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89219100; PubMed=2710135;
RA   Russell J., Sherwood L.M.;
RT   "Nucleotide sequence of the DNA complementary to avian (chicken)
RT   preproparathyroid hormone mRNA and the deduced sequence of the
RT   hormone precursor.";
RL   Mol. Endocrinol. 3:325-331(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89284968; PubMed=3251402;
RA   Khosla S., Demay M., Pines M., Hurwitz S., Potts J.T. Jr.,
RA   Kronenberg H.M.;
RT   "Nucleotide sequence of cloned cDNAs encoding chicken
RT   preproparathyroid hormone.";
RL   J. Bone Miner. Res. 3:689-698(1988).
CC   -!- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC       BONE AND PREVENTING THEIR RENAL EXCRETION.
CC   -!- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
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CC   --------------------------------------------------------------------------
DR   EMBL; M31604; AAA49093.1; -.
DR   EMBL; M36522; AAB02866.1; -.
DR   PIR; A34937; A34937.
DR   HSSP; P01270; 1HPY.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   Pfam; PF01279; Parathyroid; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   SMART; SM00087; PTH; 1.
DR   PROSITE; PS00335; PARATHYROID; 1.
KW   Hormone; Signal.
FT   SIGNAL        1     25
FT   PROPEP       26     31
FT   CHAIN        32    119       PARATHYROID HORMONE.
SQ   SEQUENCE   119 AA;  13943 MW;  B309D8E772997F6E CRC64;

  Query Match             27.1%;  Score 68.5;  DB 1;  Length 119;
  Best Local Similarity   38.9%;  Pred. No. 0.12;
  Matches   21;  Conservative    6;  Mismatches   14;  Indels   13;  Gaps    1;

Qy      9 APRDAGSQRPRKKEDNVLVE-------------SHEKSLGEANKADVNVLTKAK 49
          |  || :|||| ||| || |             : :|   : :|| :||| | |
Db     65 ALEDARTQRPRNKEDIVLGEIRNRRLLPEHLRAAVQKKSIDLDKAYMNVLFKTK 118

RESULT 8
MYH8_HUMAN
ID   MYH8_HUMAN     STANDARD;      PRT;  1937 AA.
AC   P13535; Q14910;
DT   01-JAN-1990 (Rel. 13, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Myosin heavy chain, skeletal muscle, perinatal (MyHC-perinatal).
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GN   MYH8.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skeletal muscle;
RX   MEDLINE=90323631; PubMed=2373371;
RA   Karsch-Mizrachi I., Feghali R., Shows T.B. Jr., Leinwand L.A.;
RT   "Generation of a full-length human perinatal myosin heavy-chain-
RT   encoding cDNA.";
RL   Gene 89:289-294(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skeletal muscle;
RX   MEDLINE=95324556; PubMed=7601129;
RA   Jullian E.H., Kelly A.M., Pompidou A.J., Hoffman R., Schiaffino S.,
RA   Stedman H.H., Rubinstein N.A.;
RT   "Characterization of a human perinatal myosin heavy-chain
RT   transcript.";
RL   Eur. J. Biochem. 230:1001-1006(1995).
RN   [3]
RP   SEQUENCE OF 502-1937 FROM N.A.
RC   TISSUE=Skeletal muscle;
RX   MEDLINE=90235862; PubMed=1691980;
RA   Bober E., Buchberger-Seidl A., Braun T., Singh S., Goedde H.W.,
RA   Arnold H.H.;
RT   "Identification of three developmentally controlled isoforms of human
RT   myosin heavy chains.";
RL   Eur. J. Biochem. 189:55-65(1990).
RN   [4]
RP   SEQUENCE OF 860-1937 FROM N.A.
RX   MEDLINE=89234168; PubMed=2715179;
RA   Feghali R., Leinwand L.A.;
RT   "Molecular genetic characterization of a developmentally regulated
RT   human perinatal myosin heavy chain.";
RL   J. Cell Biol. 108:1791-1797(1989).
RN   [5]
RP   SEQUENCE OF 1-46 FROM N.A.
RA   Esser K., Tidhar A., Myszkowski M.;
RT   "Isolation and characterization of the human perinatal MHC promoter.";
RL   Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: MUSCLE CONTRACTION.
CC   -!- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
CC       HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
CC       AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
CC   -!- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
CC   -!- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
CC       CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
CC       CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
CC   -!- PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY
CC       ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.
CC   -!- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
CC       MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE
CC       SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
CC       SUBFRAGMENT (S2).
CC   -!- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 IQ DOMAIN.
CC   --------------------------------------------------------------------------
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CC   --------------------------------------------------------------------------
DR   EMBL; M36769; AAC17185.1; -.
DR   EMBL; Z38133; CAA86293.1; -.
DR   EMBL; X51592; CAA35941.1; -.
DR   EMBL; AF067143; AAC21557.1; -.
DR   PIR; A30220; A30220.
DR   HSSP; P13538; 2MYS.
DR   Genew; HGNC:7578; MYH8.
DR   MIM; 160741; -.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR004009; Myosin_N.
DR   InterPro; IPR002928; Myosin_tail.
DR   InterPro; IPR001609; myosin_head.
DR   Pfam; PF00063; myosin_head; 1.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF01576; Myosin_tail; 1.
DR   Pfam; PF02736; Myosin_N; 1.
DR   PRINTS; PR00193; MYOSINHEAVY.
DR   ProDom; PD000355; myosin_head; 1.
DR   SMART; SM00015; IQ; 1.
DR   SMART; SM00242; MYSc; 1.
DR   PROSITE; PS50096; IQ; 1.
KW   Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding;
KW   ATP-binding; Methylation; Alkylation; Multigene family;
KW   Calmodulin-binding.
FT   DOMAIN        1    780       MYOSIN HEAD-LIKE.
FT   DOMAIN      781    813       IQ.
FT   DOMAIN      842   1937       COILED COIL (POTENTIAL).
FT   NP_BIND     181    188       ATP.
FT   DOMAIN      658    680       ACTIN-BINDING.
FT   DOMAIN      760    774       ACTIN-BINDING.
FT   MOD_RES     132    132       METHYLATION (TRI-) (POTENTIAL).
FT   MOD_RES     698    698       ALKYLATION (SH-1) (POTENTIAL).
FT   MOD_RES     708    708       ALKYLATION (SH-2) (POTENTIAL).
FT   CONFLICT     15     15       A -> R (IN REF. 2).
FT   CONFLICT    970    970       E -> Q (IN REF. 1 AND 4).
FT   CONFLICT   1072   1072       M -> N (IN REF. 3).
FT   CONFLICT   1247   1247       N -> H (IN REF. 1 AND 4).
FT   CONFLICT   1251   1252       MC -> DGG (IN REF. 3).
FT   CONFLICT   1261   1261       E -> G (IN REF. 1 AND 4).
FT   CONFLICT   1297   1297       K -> Q (IN REF. 1 AND 4).
FT   CONFLICT   1377   1378       KY -> NT (IN REF. 3).
FT   CONFLICT   1504   1505       EN -> AH (IN REF. 1 AND 4).
FT   CONFLICT   1847   1847       E -> D (IN REF. 1 AND 4).
FT   CONFLICT   1914   1914       D -> H (IN REF. 2).
SQ   SEQUENCE   1937 AA;  222762 MW;  A3EE2D151792E9E8 CRC64;

  Query Match             24.9%;  Score 63;  DB 1;  Length 1937;
  Best Local Similarity   42.4%;  Pred. No. 14;
  Matches   14;  Conservative    9;  Mismatches    8;  Indels    2;  Gaps    1;

Qy     21 KEDNVLVESHEKSLG--EANKADVNVLTKAKSQ 51
          ||   | |:|:::|   :| :  ||:|||||::
Db    997 KEKKALQETHQQTLDDLQAEEDKVNILTKAKTK 1029


RESULT 9
YE05_HAEIN
ID   YE05_HAEIN     STANDARD;      PRT;   366 AA.
AC   P44180;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Hypothetical protein HI1405.
GN   HI1405.
OS   Haemophilus influenzae.
OC   Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC   Haemophilus.
OX   NCBI_TaxID=727;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Rd / KW20 / ATCC 51907;
RX   MEDLINE=95350630; PubMed=7542800;
RA   Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA   Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA   McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA   Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA   Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA   Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
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RA   Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA   Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA   Venter J.C.;
RT   "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT   Rd.";
RL   Science 269:496-512(1995).
CC   --------------------------------------------------------------------------
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CC   --------------------------------------------------------------------------
DR   EMBL; U32820; AAC23055.1; -.
DR   TIGR; HI1405; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   366 AA;  40122 MW;  68040800B631AEC0 CRC64;

  Query Match             24.3%;  Score 61.5;  DB 1;  Length 366;
  Best Local Similarity   35.6%;  Pred. No. 3.2;
  Matches   16;  Conservative   10;  Mismatches   18;  Indels    1;  Gaps    1;

Qy      7 PLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
          |  |::  |:   ||||:|  |  |||| :|   ::  |  |:::
Db    222 PTKPKEKKSEPENKKEDDVEKEELEKSL-KAKDEEIQQLKDAQAK 265


RESULT 10
UL25_HSV6Z
ID   UL25_HSV6Z     STANDARD;      PRT;   555 AA.
AC   P52537;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Virion protein U50.
GN   U50 OR KA11R.
OS   Human herpesvirus (type 6 / strain Z29) (HHV6).
OC   Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC   Betaherpesvirinae; Roseolovirus.
OX   NCBI_TaxID=36351;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95074921; PubMed=7983761;
RA   Stamey F.R., Dominguez G., Black J.B., Dambaugh T.R., Pellett P.E.;
RT   "Intragenomic linear amplification of human herpesvirus 6B oriLyt
RT   suggests acquisition of oriLyt by transposition.";
RL   J. Virol. 69:589-596(1995).
CC   -!- FUNCTION: VIRION PROTEIN.
CC   -!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL25,
CC       EHV-1 36, EBV BVRF1, HCMV UL77, ILTV ORF2, AND VZV 34.
CC   --------------------------------------------------------------------------
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CC   --------------------------------------------------------------------------
DR   EMBL; AF157706; AAB06348.1; -.
DR   InterPro; IPR002493; UL25.
DR   Pfam; PF01499; UL25; 1.
SQ   SEQUENCE   555 AA;  63830 MW;  68B86590DC4CD2BC CRC64;

  Query Match             23.9%;  Score 60.5;  DB 1;  Length 555;
  Best Local Similarity   42.5%;  Pred. No. 6.8;
  Matches   17;  Conservative    8;  Mismatches   10;  Indels    5;  Gaps    2;

Qy     16 QRPRKKEDNVLVESHEKSLGEA----NKADVNVLTKAKSQ 51
          ||  :|: :||  || |:: :|    |  :||| ||| :|
Db     67 QRKMQKDSDVL-NSHLKAIEDALLFTNDGEVNVETKADTQ 105
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RESULT 11
MYSS_RABIT
ID   MYSS_RABIT     STANDARD;      PRT;  1084 AA.
AC   P02562;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   Myosin heavy chain, skeletal muscle (Fragments).
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE OF 1-258.
RA   Capony J.-P., Elzinga M.;
RT   "The amino acid sequence of A 34,000 dalton fragment from S-2 of
RT   myosin.";
RL   Biophys. J. 33:148A-148A(1981).
RN   [2]
RP   SEQUENCE OF 259-428.
RX   MEDLINE=85131142; PubMed=3972832;
RA   Lu R.C., Wong A.;
RT   "The amino acid sequence and stability predictions of the hinge
RT   region in myosin subfragment 2.";
RL   J. Biol. Chem. 260:3456-3461(1985).
RN   [3]
RP   SEQUENCE OF 409-1084 FROM N.A.
RX   MEDLINE=87304245; PubMed=3305014;
RA   Maeda K., Sczakiel G., Wittinghofer A.;
RT   "Characterization of cDNA coding for the complete light meromyosin
RT   portion of a rabbit fast skeletal muscle myosin heavy chain.";
RL   Eur. J. Biochem. 167:97-102(1987).
CC   -!- FUNCTION: MUSCLE CONTRACTION.
CC   -!- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
CC       HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
CC       AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
CC   -!- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
CC   -!- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
CC       CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
CC       CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
CC   -!- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
CC       MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE
CC       SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
CC       SUBFRAGMENT (S2).
CC   -!- SIMILARITY: THE PERIODICITIES OF HYDROPHOBIC AND CHARGED RESIDUES,
CC       WHICH DICTATE THE ALPHA-HELICAL COILED-COIL STRUCTURE ARE
CC       CONSERVED.
CC   --------------------------------------------------------------------------
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CC   --------------------------------------------------------------------------
DR   EMBL; X05958; CAA29391.1; -.
DR   PIR; A02985; A02985.
DR   PIR; A05280; A05280.
DR   PIR; S00084; S00084.
KW   Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding;
KW   ATP-binding; Multigene family.
FT   NON_TER       1      1
FT   DOMAIN       <1   >258       ALPHA-HELICAL TAILPIECE (S2).
FT   NON_CONS    258    259
FT   DOMAIN     <259   1084       RODLIKE TAIL (S2 AND LMM DOMAINS).
FT   DOMAIN      455   1084       COILED COIL (POTENTIAL).
FT   VARIANT     405    405       L -> V.
FT   VARIANT     408    408       V -> L.
FT   VARIANT     421    421       E -> D.
FT   VARIANT     423    423       S -> G.
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FT   VARIANT     426    426       K -> R.
SQ   SEQUENCE   1084 AA;  125488 MW;  229CFD69A6E1F7F0 CRC64;

  Query Match             23.7%;  Score 60;  DB 1;  Length 1084;
  Best Local Similarity   42.4%;  Pred. No. 17;
  Matches   14;  Conservative    8;  Mismatches    9;  Indels    2;  Gaps    1;

Qy       21 KEDNVLVESHEKSLG--EANKADVNVLTKAKSQ 51
            ||   | |:|:::|   :| :  || |||||::
Db      152 KEKKALQEAHQQTLDDLQAEEDKVNTLTKAKTK 184


RESULT 12
MYSS_CYPCA
ID   MYSS_CYPCA     STANDARD;      PRT;  1935 AA.
AC   Q90339;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Myosin heavy chain, fast skeletal muscle.
OS   Cyprinus carpio (Common carp).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Cyprinus.
OX   NCBI_TaxID=7962;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Fast muscle;
RX   MEDLINE=97352533; PubMed=9208928;
RA   Hirayama Y., Watabe S.;
RT   "Structural differences in the crossbridge head of temperature-
RT   associated myosin subfragment-1 isoforms from carp fast skeletal
RT   muscle.";
RL   Eur. J. Biochem. 246:380-387(1997).
RN   [2]
RP   SEQUENCE OF 981-1935 FROM N.A.
RC   TISSUE=Fast muscle;
RX   MEDLINE=97176447; PubMed=9023993;
RA   Imai J., Hirayama Y., Kikuchi K., Kakinuma M., Watabe S.;
RT   "cDNA cloning of myosin heavy chain isoforms from carp fast skeletal
RT   muscle and their gene expression associated with temperature
RT   acclimation.";
RL   J. Exp. Biol. 200:27-34(1997).
RN   [3]
RP   SEQUENCE OF 1387-1528 FROM N.A.
RX   MEDLINE=95194396; PubMed=7887920;
RA   Watabe S., Imai J., Nakaya M., Hirayama Y., Okamoto Y., Masaki H.,
RA   Uozumi T., Hirono I., Aoki T.;
RT   "Temperature acclimation induces light meromyosin isoforms with
RT   different primary structures in carp fast skeletal muscle.";
RL   Biochem. Biophys. Res. Commun. 208:118-125(1995).
CC   -!- FUNCTION: MUSCLE CONTRACTION.
CC   -!- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
CC       HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
CC       AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
CC   -!- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
CC   -!- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
CC       CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
CC       CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
CC   -!- PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY
CC       ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.
CC   -!- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
CC       MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE
CC       SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
CC       SUBFRAGMENT (S2).
CC   -!- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 IQ DOMAIN.
CC   --------------------------------------------------------------------------
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CC   modified and this statement is not removed.  Usage  by  and for commercial
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; D89992; BAA22069.1; -.
DR   EMBL; D50476; BAA09069.1; -.
DR   EMBL; D43700; BAA07802.1; -.
DR   HSSP; P13538; 2MYS.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR004009; Myosin_N.
DR   InterPro; IPR002928; Myosin_tail.
DR   InterPro; IPR001609; myosin_head.
DR   Pfam; PF00063; myosin_head; 1.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF01576; Myosin_tail; 1.
DR   Pfam; PF02736; Myosin_N; 1.
DR   PRINTS; PR00193; MYOSINHEAVY.
DR   ProDom; PD000355; myosin_head; 1.
DR   SMART; SM00015; IQ; 1.
DR   SMART; SM00242; MYSc; 1.
DR   PROSITE; PS50096; IQ; 1.
KW   Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding;
KW   ATP-binding; Methylation; Alkylation; Calmodulin-binding;
KW   Multigene family.
FT   DOMAIN        1    781       MYOSIN HEAD-LIKE.
FT   DOMAIN      782    811       IQ.
FT   DOMAIN      812    839       HINGE.
FT   DOMAIN      840   1935       COILED COIL (POTENTIAL).
FT   NP_BIND     178    185       ATP (POTENTIAL).
FT   DOMAIN      659    681       ACTIN-BINDING.
FT   DOMAIN      761    775       ACTIN-BINDING.
FT   MOD_RES     129    129       METHYLATION (TRI-) (POTENTIAL).
FT   MOD_RES     699    699       ALKYLATION (SH-1).
FT   MOD_RES     709    709       ALKYLATION (SH-2).
SQ   SEQUENCE   1935 AA;  221599 MW;  9A1244B67D63C83B CRC64;

  Query Match             23.7%;  Score 60;  DB 1;  Length 1935;
  Best Local Similarity   42.4%;  Pred. No. 32;
  Matches   14;  Conservative    8;  Mismatches    9;  Indels    2;  Gaps    1;

Qy       21 KEDNVLVESHEKSLG--EANKADVNVLTKAKSQ 51
            ||   | |:|:::|   :| :  || |||||::
Db      995 KEKKALQEAHQQTLDDLQAEEDKVNTLTKAKTK 1027


RESULT 13
MYH4_RABIT
ID   MYH4_RABIT     STANDARD;      PRT;  1938 AA.
AC   Q28641;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Myosin heavy chain, skeletal muscle, juvenile.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=New Zealand white; TISSUE=Skeletal muscle;
RA   Maeda K., Hostinova E., Roesch-Kleinkauf A., Schuster H., Gasperik J.,
RA   Wittinghofer A.;
RT   "Isolation, sequencing of myosin heavy chain cDNA from rabbit
RT   skeletal muscle and a novel cosynthesis of S-1 fragment with the
RT   essential and regulatory light chains.";
RL   Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: MUSCLE CONTRACTION.
CC   -!- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
CC       HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
CC       AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
CC   -!- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
CC   -!- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
CC       CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
CC       CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
```

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CC   -!- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
CC       MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE
CC       SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
CC       SUBFRAGMENT (S2).
CC   -!- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 IQ DOMAIN.
CC   --------------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; U32574; AAA74199.1; -.
DR   HSSP; P13538; 2MYS.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR004009; Myosin_N.
DR   InterPro; IPR002928; Myosin_tail.
DR   InterPro; IPR001609; myosin_head.
DR   Pfam; PF00063; myosin_head; 1.
DR   Pfam; PF00612; IQ; 2.
DR   Pfam; PF01576; Myosin_tail; 1.
DR   Pfam; PF02736; Myosin_N; 1.
DR   PRINTS; PR00193; MYOSINHEAVY.
DR   ProDom; PD000355; myosin_head; 1.
DR   SMART; SM00015; IQ; 1.
DR   SMART; SM00242; MYSc; 1.
DR   PROSITE; PS50096; IQ; 1.
KW   Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding;
KW   Calmodulin-binding; ATP-binding; Methylation; Alkylation;
KW   Multigene family.
FT   DOMAIN        1    783       MYOSIN HEAD-LIKE.
FT   DOMAIN      784    813       IQ.
FT   DOMAIN      842   1938       COILED COIL (POTENTIAL).
FT   NP_BIND     179    186       ATP (POTENTIAL).
FT   DOMAIN      658    680       ACTIN-BINDING (BY SIMILARITY).
FT   DOMAIN      760    774       ACTIN-BINDING (BY SIMILARITY).
FT   MOD_RES      35     35       METHYLATION (MONO-) (BY SIMILARITY).
FT   MOD_RES     130    130       METHYLATION (TRI-) (BY SIMILARITY).
FT   MOD_RES     552    552       METHYLATION (TRI-) (BY SIMILARITY).
FT   MOD_RES     756    756       METHYLATION (TRI-) (BY SIMILARITY).
FT   MOD_RES     698    698       ALKYLATION (SH-1) (BY SIMILARITY).
FT   MOD_RES     708    708       ALKYLATION (SH-2) (BY SIMILARITY).
SQ   SEQUENCE   1938 AA;  223064 MW;  D8A8A2EC5B182626 CRC64;

  Query Match             23.7%;  Score 60;  DB 1;  Length 1938;
  Best Local Similarity   42.4%;  Pred. No. 32;
  Matches   14;  Conservative    8;  Mismatches    9;  Indels    2;  Gaps    1;

Qy     21 KEDNVLVESHEKSLG--EANKADVNVLTKAKSQ 51
          ||   | |:|:::|   :| :  || |||||::
Db    997 KEKKALQEAHQQTLDDLQAEEDKVNTLTKAKTK 1029


RESULT 14
MYH3_CHICK
ID   MYH3_CHICK     STANDARD;      PRT;  1940 AA.
AC   P02565;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Myosin heavy chain, fast skeletal muscle, embryonic.
GN   MYH3.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87194881; PubMed=3571266;
RA   Molina M.I., Kropp K.E., Gulick J., Robbins J.;
RT   "The sequence of an embryonic myosin heavy chain gene and isolation
RT   of its corresponding cDNA.";
RL   J. Biol. Chem. 262:6478-6488(1987).
RN   [2]
RP   SEQUENCE OF 1502-1940 FROM N.A.
RX   MEDLINE=83161144; PubMed=6833296;
RA   Kavinsky C.J., Umeda P.K., Sinha A.M., Elzinga M., Tong S.W., Zak R.,
RA   Jakovcic S., Rabinowitz M.;
RT   "Cloned mRNA sequences for two types of embryonic myosin heavy chains
RT   from chick skeletal muscle. I. DNA and derived amino acid sequence of
RT   light meromyosin.";
RL   J. Biol. Chem. 258:5196-5205(1983).
CC   -!- FUNCTION: MUSCLE CONTRACTION.
CC   -!- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
CC       HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
CC       AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
CC   -!- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
CC   -!- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
CC       CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
CC       CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
CC   -!- PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY
CC       ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.
CC   -!- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
CC       MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE
CC       SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
CC       SUBFRAGMENT (S2).
CC   -!- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 IQ DOMAIN.
CC   --------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; V00430; CAA23712.1; -.
DR   EMBL; J02714; AAA48972.1; -.
DR   PIR; A02990; A02990.
DR   PIR; A29320; A29320.
DR   HSSP; P13538; 2MYS.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR004009; Myosin_N.
DR   InterPro; IPR002928; Myosin_tail.
DR   InterPro; IPR001609; myosin_head.
DR   Pfam; PF00063; myosin_head; 1.
DR   Pfam; PF00612; IQ; 2.
DR   Pfam; PF01576; Myosin_tail; 1.
DR   Pfam; PF02736; Myosin_N; 1.
DR   PRINTS; PR00193; MYOSINHEAVY.
DR   ProDom; PD000355; myosin_head; 1.
DR   SMART; SM00015; IQ; 1.
DR   SMART; SM00242; MYSc; 1.
DR   PROSITE; PS50096; IQ; 1.
KW   Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding;
KW   Calmodulin-binding; ATP-binding; Methylation; Alkylation;
KW   Multigene family.
FT   DOMAIN        1    785       MYOSIN HEAD-LIKE.
FT   DOMAIN      786    815       IQ.
FT   DOMAIN      844   1940       COILED COIL (POTENTIAL).
FT   NP_BIND     179    186       ATP.
FT   DOMAIN      660    682       ACTIN-BINDING.
FT   DOMAIN      762    776       ACTIN-BINDING.
FT   MOD_RES     130    130       METHYLATION (TRI-) (POTENTIAL).
FT   MOD_RES     700    700       ALKYLATION (SH-1).
FT   MOD_RES     710    710       ALKYLATION (SH-2).
FT   VARIANT     379    379       G -> D.
FT   CONFLICT   1547   1547       T -> A (IN REF. 2).
FT   CONFLICT   1913   1915       ERA -> GRT (IN REF. 2).
SQ   SEQUENCE   1940 AA;  222816 MW;  C34833D75B04DFF2 CRC64;
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  Query Match             23.7%;  Score 60;  DB 1;  Length 1940;
  Best Local Similarity   42.4%;  Pred. No. 33;
  Matches   14;  Conservative    8;  Mismatches    9;  Indels    2;  Gaps    1;

Qy     21 KEDNVLVESHEKSLG--EANKADVNVLTKAKSQ 51
          ||   | |:|:::|   :| :  || |||||::
Db    999 KEKKALQEAHQQTLDDLQAEEDKVNTLTKAKTK 1031


RESULT 15
ATRX_RAT
ID   ATRX_RAT       STANDARD;      PRT;   527 AA.
AC   P70486;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Transcriptional regulator ATRX (X-linked nuclear protein) (pABP-2)
DE   (Fragment).
GN   ATRX.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC   STRAIN=Wistar; TISSUE=Embryonic brain;
RX   MEDLINE=96301899; PubMed=8667030;
RA   Ohsawa K., Imai Y., Ito D., Kohsaka S.;
RT   "Molecular cloning and characterization of annexin V-binding proteins
RT   with highly hydrophilic peptide structure.";
RL   J. Neurochem. 67:89-97(1996).
CC   -!- FUNCTION: COULD BE A GLOBAL TRANSCRIPTIONAL REGULATOR. MODIFIES
CC       GENE EXPRESSION BY AFFECTING CHROMATIN.
CC   -!- SUBUNIT: PROBABLY BINDS EZH2. BINDS ANNEXIN V IN A CALCIUM AND
CC       PHOSPHATIDYLCHOLINE/PHOSPHATIDYLSERINE-DEPENDENT MANNER.
CC   -!- SUBCELLULAR LOCATION: NUCLEAR. ASSOCIATED WITH PERICENTROMERIC
CC       HETEROCHROMATIN DURING INTERPHASE AND MITOSIS, PROBABLY BY
CC       INTERACTING WITH HP1 (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE SNF2/RAD54 HELICASE FAMILY.
CC   --------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; D64059; BAA10936.1; -.
KW   DNA repair; Nuclear protein; DNA-binding; Helicase.
FT   NON_TER       1      1
FT   DOMAIN      251    256       POLY-SER.
FT   DOMAIN      304    307       POLY-SER.
FT   DOMAIN      360    367       POLY-ASP.
FT   NON_TER     527    527
SQ   SEQUENCE   527 AA;  59258 MW;  ABEF4B10C086D638 CRC64;

  Query Match             23.1%;  Score 58.5;  DB 1;  Length 527;
  Best Local Similarity   33.9%;  Pred. No. 11;
  Matches   19;  Conservative    7;  Mismatches   17;  Indels   13;  Gaps    2;

Qy      9 APRDAGSQRPRKKEDNV-------LVESHEKS------LGEANKADVNVLTKAKSQ 51
          |   |||::|  ||:||       : :| |||       |   |:||    : | |
Db     18 AVSSAGSEKPSGKEENVHSPEDKRVTKSKEKSKHLRTRTGRKVKSDVTDRFRKKEQ 73


Search completed: March 13, 2003, 15:00:51
Job time : 6.70896 secs
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                     GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on:         March 13, 2003, 14:57:54 ; Search time 19.791 Seconds
                                           (without alignments)
                                           530.968 Million cell updates/sec

Title:          US-09-636-530-3
Perfect score:  253
Sequence:       1 FVALGAPLAPRDAGSQRPRK..........KSLGEANKADVNVLTKAKSQ 51

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters:      671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       SPTREMBL_21:*
                1:  sp_archea:*
                2:  sp_bacteria:*
                3:  sp_fungi:*
                4:  sp_human:*
                5:  sp_invertebrate:*
                6:  sp_mammal:*
                7:  sp_mhc:*
                8:  sp_organelle:*
                9:  sp_phage:*
                10:  sp_plant:*
                11:  sp_rodent:*
                12:  sp_virus:*
                13:  sp_vertebrate:*
                14:  sp_unclassified:*
                15:  sp_rvirus:*
                16:  sp_bacteriap:*
                17:  sp_archeap:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

                               SUMMARIES
                  %
Result            Query
  No.   Score   Match Length  DB  ID                  Description
-------------------------------------------------------------------------
    1    205    81.0     115  6  Q9GL67               Q9gl67 felis silve
    2    203    80.2      86  6  Q9N1V0               Q9n1v0 equus cabal
    3    158    62.5     115  11  Q9Z0L6               Q9z0l6 mus musculu
    4     65    25.7     283  9  Q9AZW5               Q9azw5 bacteriopha
    5     65    25.7     283  16  Q9CFN5               Q9cfn5 lactococcus
    6   63.5    25.1     487  10  O23304               O23304 arabidopsis
    7     63    24.9     975  13  Q98TQ5               Q98tq5 notothenia
    8     63    24.9    1119  13  P87344               P87344 theragra ch
    9     63    24.9    1287  13  O93498               O93498 theragra ch
   10     63    24.9    1929  13  Q98TQ6               Q98tq6 notothenia
   11     61    24.1     565  16  Q99WC5               Q99wc5 staphylococ
   12     60    23.7    1092  13  Q90338               Q90338 cyprinus ca
   13     60    23.7    1930  13  Q9DGD5               Q9dgd5 pennahia ar
   14     60    23.7    1931  13  O42352               O42352 cyprinus ca
   15     60    23.7    1931  13  Q910C5               Q910c5 gallus gall
   16     60    23.7    1933  13  Q90337               Q90337 cyprinus ca
   17     60    23.7    1936  13  Q90YF6               Q90yf6 paracirrhit
   18     60    23.7    1937  6  Q9TV62               Q9tv62 sus scrofa
   19     60    23.7    1938  6  Q9BE40               Q9be40 bos taurus
   20     60    23.7    1938  13  Q9IBD7               Q9ibd7 seriola dum
   21     60    23.7    1939  6  Q9TV63               Q9tv63 sus scrofa
   22     60    23.7    1939  6  Q9TV61               Q9tv61 sus scrofa
   23     60    23.7    1940  6  Q9BE41               Q9be41 bos taurus
   24     60    23.7    1941  13  Q9DGM4               Q9dgm4 gallus gall
   25     60    23.7    1944  13  Q9DGM5               Q9dgm5 gallus gall
   26     60    23.7    5170  5  Q17490               Q17490 caenorhabdi
   27     60    23.7    6994  5  Q17343               Q17343 caenorhabdi
   28   59.5    23.5     909  2  Q52585               Q52585 pseudomonas
   29   59.5    23.5    1400  5  Q9TYW5               Q9tyw5 caenorhabdi
   30     59    23.3     462  2  O05090               O05090 nocardioide
   31     59    23.3    1006  4  Q96I57               Q96i57 homo sapien
   32     59    23.3    1692  4  Q9P216               Q9p216 homo sapien
   33     59    23.3    1889  4  Q9H430               Q9h430 homo sapien
   34   58.5    23.1     142  10  Q9M344               Q9m344 arabidopsis
   35   58.5    23.1     288  10  Q94GU9               Q94gu9 oryza sativ
   36     58    22.9     234  6  Q28829               Q28829 oryctolagus
   37     58    22.9     258  4  Q92679               Q92679 homo sapien
   38     58    22.9     518  5  Q9VRP4               Q9vrp4 drosophila
   39     58    22.9     619  11  Q91YS4               Q91ys4 mus musculu
   40     58    22.9    1038  6  Q28699               Q28699 oryctolagus
   41     58    22.9    1598  11  Q922D2               Q922d2 mus musculu
   42     58    22.9    1935  4  Q9H1D5               Q9h1d5 homo sapien
   43     58    22.9    1935  6  Q9GKR1               Q9gkr1 sus scrofa
   44     58    22.9    1935  6  Q9BE39               Q9be39 bos taurus
   45     58    22.9    1935  11  Q91Z83               Q91z83 mus musculu


                               ALIGNMENTS


RESULT 1
Q9GL67
ID   Q9GL67     PRELIMINARY;      PRT;   115 AA.
AC   Q9GL67;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Preproparathyroid hormone precursor.
GN   PTH.
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Toribio R.E., Kohn C.W., Leone G.W., Capen C.C., Rosol T.J.;
RT   "Molecular cloning of feline preproparathyroid hormone.";
RL   Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF309967; AAG30545.1; -.
DR   HSSP; P01268; 1ZWC.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   Pfam; PF01279; Parathyroid; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   SMART; SM00087; PTH; 1.
DR   PROSITE; PS00335; PARATHYROID; 1.
KW   Signal.
FT   SIGNAL        1     25       POTENTIAL.
FT   CHAIN        32    115       PARATHYROID HORMONE.
SQ   SEQUENCE   115 AA;  12921 MW;  80CD557CC6A1A47E CRC64;

  Query Match             81.0%;  Score 205;  DB 6;  Length 115;
  Best Local Similarity   80.4%;  Pred. No. 9.9e-18;
  Matches   41;  Conservative    5;  Mismatches    5;  Indels    0;  Gaps    0;

Qy      1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
          |||||||:| || ||||||||||||  |:|:||||||:||||:|| |||||
Db     65 FVALGAPIAHRDGGSQRPRKKEDNVPAENHQKSLGEADKADVDVLIKAKSQ 115
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RESULT 2
Q9N1V0
ID   Q9N1V0      PRELIMINARY;      PRT;    86 AA.
AC   Q9N1V0;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Parathyroid hormone (Fragment).
GN   PTH.
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20082971; PubMed=10613847;
RA   Caetano A.R., Shiue Y.L., Lyons L.A., O'Brien S.J., Laughlin T.F.,
RA   Bowling A.T., Murray J.D.;
RT   "A comparative gene map of the horse (Equus caballus).";
RL   Genome Res. 9:1239-1249(1999).
DR   EMBL; AF134233; AAF62347.1; -.
DR   HSSP; P01270; 1HPY.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   Pfam; PF01279; Parathyroid; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   SMART; SM00087; PTH; 1.
DR   PROSITE; PS00335; PARATHYROID; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   86 AA;  9805 MW;  253184EA681A2022 CRC64;

  Query Match              80.2%;  Score 203;  DB 6;  Length 86;
  Best Local Similarity    76.5%;  Pred. No. 1.3e-17;
  Matches   39;  Conservative    7;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
           |:|||||:  || |||||||||||||:|||: |||||:||||:||:| |||
Db      36 FIALGAPIFHRDGGSQRPRKKEDNVLIESHQXSLGEADKADVDVLSKTKSQ 86


RESULT 3
Q9Z0L6
ID   Q9Z0L6      PRELIMINARY;      PRT;   115 AA.
AC   Q9Z0L6;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Parathyroid hormone precursor.
GN   PTH.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SV;
RA   Karaplis A.C., He B., Hiou-Tim F.F.T., Al-Akad B., Kronenberg H.M.;
RT   "Cloning of the murine gene encoding parathyroid hormone: genomic
RT   organization and nucleotide sequence.";
RL   Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF066075; AAC99656.1; -.
DR   HSSP; P01270; 1ZWB.
DR   MGD; MGI:97799; Pth.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   Pfam; PF01279; Parathyroid; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   SMART; SM00087; PTH; 1.
DR   PROSITE; PS00335; PARATHYROID; 1.
KW   Signal.
FT   SIGNAL        1     25       POTENTIAL.
FT   CHAIN        32    115       PARATHYROID HORMONE.
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SQ   SEQUENCE   115 AA;  12825 MW;  DA43FABBCB4E2FD9 CRC64;

  Query Match              62.5%;  Score 158;  DB 11;  Length 115;
  Best Local Similarity    60.8%;  Pred. No. 6.3e-12;
  Matches   31;  Conservative    9;  Mismatches   11;  Indels    0;  Gaps    0;

Qy       1 FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
           ||:||  :| ||   |:| |||:||||: : ||||| :||||:|| |:|||
Db      65 FVSLGVQMAARDGSHQKPTKKEENVLVDGNPKSLGEGDKADVDVLVKSKSQ 115


RESULT 4
Q9AZW5
ID   Q9AZW5      PRELIMINARY;      PRT;   283 AA.
AC   Q9AZW5;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Orf2.
GN   ORF2.
OS   bacteriophage bIL286.
OC   Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX   NCBI_TaxID=151536;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21113149; PubMed=11160885;
RA   Chopin A., Bolotin A., Sorokin A., Ehrlich S.D., Chopin M.-C.;
RT   "Analysis of six prophages in Lactococcus lactis IL1403: different
RT   genetic structure of temperate and virulent phage populations.";
RL   Nucleic Acids Res. 29:644-651(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Chopin A., Bolotin A., Sorokin A., Ehrlich S.D., Chopin M.-C.;
RL   Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF323669; AAK08289.1; -.
SQ   SEQUENCE   283 AA;  31164 MW;  DF4094313735E02A CRC64;

  Query Match              25.7%;  Score 65;  DB 9;  Length 283;
  Best Local Similarity    36.1%;  Pred. No. 5.2;
  Matches   13;  Conservative    8;  Mismatches   15;  Indels    0;  Gaps    0;

Qy      15 SQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKS 50
           |:  :| : |:|::|  | : : | ||  ||   ||
Db     110 SKESKKSDSNLLIDSQYKEIADENGADSAVLVATKS 145


RESULT 5
Q9CFN5
ID   Q9CFN5      PRELIMINARY;      PRT;   283 AA.
AC   Q9CFN5;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Prophage pi3 protein 59.
GN   PI359 OR LL1432.
OS   Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC   Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC   Streptococcaceae; Lactococcus.
OX   NCBI_TaxID=1360;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=IL1403;
RX   MEDLINE=21235186; PubMed=11337471;
RA   Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K.,
RA   Weissenbach J., Ehrlich S.D., Sorokin A.;
RT   "The complete genome sequence of the lactic acid bacterium Lactococcus
RT   lactis ssp. lactis IL1403.";
RL   Genome Res. 11:731-753(2001).
DR   EMBL; AE006373; AAK05530.1; -.
KW   Complete proteome.
SQ   SEQUENCE   283 AA;  31164 MW;  DF4094313735E02A CRC64;

  Query Match              25.7%;  Score 65;  DB 16;  Length 283;
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  Best Local Similarity   36.1%;  Pred. No. 5.2;
  Matches   13;  Conservative    8;  Mismatches   15;  Indels    0;  Gaps    0;

Qy     15 SQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKS 50
          |:  :| : |:|::|  | : : | ||  ||   ||
Db    110 SKESKKSDSNLLIDSQYKEIADENGADSAVLVATKS 145


RESULT 6
O23304
ID   O23304      PRELIMINARY;      PRT;   487 AA.
AC   O23304;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   STE20-like kinase homolog (Kinase like protein).
GN   AT4G14480.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Bevan M., Stiekema W., Murphy G., Wambutt R., Pohl T., Terryn N.,
RA   Kreis M., Kavanagh T., Entian K.D., Rieger M., James R.,
RA   Puigdomenech P., Hatzopoulos P., Obermaier B., Duesterhoft A.,
RA   Jones J., Palme K., Ansorge W., Delseny M., Bancroft I., Mewes H.W.,
RA   Schueller C., Chalwatzis N.;
RL   Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   EU Arabidopsis sequencing project;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; Z97336; CAB10227.1; -.
DR   EMBL; AL161539; CAB78490.1; -.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   ProDom; PD000001; Euk_pkinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   ATP-binding; Transferase.
SQ   SEQUENCE   487 AA;  54380 MW;  77D21D39D2FB4F20 CRC64;

  Query Match             25.1%;  Score 63.5;  DB 10;  Length 487;
  Best Local Similarity   30.2%;  Pred. No. 14;
  Matches   13;  Conservative   12;  Mismatches   11;  Indels    7;  Gaps    1;

Qy      9 APRDAGSQRPRKKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 51
          :||:    : :|::||| :  :|  || :|:       :||:|
Db    374 SPREEDQSKDKKEDDNVTITGYELGLGLSNE-------EAKNQ 409


RESULT 7
Q98TQ5
ID   Q98TQ5      PRELIMINARY;      PRT;   975 AA.
AC   Q98TQ5;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Myosin heavy chain (Fragment).
GN   MYOHC-A3 GENE.
OS   Notothenia coriiceps (black rockcod).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
OC   Notothenioidei; Nototheniidae; Notothenia.
OX   NCBI_TaxID=8208;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Gauvry L., Ennion S., Ettelaie C., Goldspink G.;
RT   "Characterisation of red and white muscle myosin heavy chain gene
RT   coding sequences from Antarctic and tropical fish.";
RL   Comp. Biochem. Physiol. 127:575-588(2000).
DR   EMBL; AJ243768; CAC27777.1; -.
DR   HSSP; P03437; 1HTM.
DR   InterPro; IPR002928; Myosin_tail.
DR   InterPro; IPR000533; Tropomyosin.
DR   Pfam; PF01576; Myosin_tail; 1.
DR   PRINTS; PR00194; TROPOMYOSIN.
FT   NON_TER       1      1
SQ   SEQUENCE   975 AA;  112313 MW;  2F7AD46A3419537F CRC64;

  Query Match             24.9%;  Score 63;  DB 13;  Length 975;
  Best Local Similarity   45.5%;  Pred. No. 36;
  Matches   15;  Conservative    7;  Mismatches    9;  Indels    2;  Gaps    1;

Qy     21 KEDNVLVESHEKSLG--EANKADVNVLTKAKSQ 51
          ||   | |||:::|   :| :  || |||||::
Db     34 KEKKALQESHQQTLDDLQAEEDKVNTLTKAKTK 66


RESULT 8
P87344
ID   P87344      PRELIMINARY;      PRT;  1119 AA.
AC   P87344;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Myosin heavy chain (Fragment).
OS   Theragra chalcogramma.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Theragra.
OX   NCBI_TaxID=48550;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=FAST MUSCLE;
RA   Togashi M., Hirayama Y., Kakinuma M., Watabe S., Ojima T., Nishita K.;
RT   "cDNA cloning of Alaska polack fast skeletal muscle myosin heavy
RT   chain.";
RL   Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB000214; BAA19070.1; -.
DR   HSSP; P13538; 2MYS.
DR   InterPro; IPR002928; Myosin_tail.
DR   InterPro; IPR000533; Tropomyosin.
DR   Pfam; PF01576; Myosin_tail; 1.
DR   PRINTS; PR00194; TROPOMYOSIN.
FT   NON_TER       1      1
SQ   SEQUENCE   1119 AA;  128626 MW;  B8C5FECAE6F5B954 CRC64;

  Query Match             24.9%;  Score 63;  DB 13;  Length 1119;
  Best Local Similarity   45.5%;  Pred. No. 42;
  Matches   15;  Conservative    7;  Mismatches    9;  Indels    2;  Gaps    1;

Qy     21 KEDNVLVESHEKSLG--EANKADVNVLTKAKSQ 51
          ||   | |||:::|   :| :  || |||||::
Db    178 KEKKALQESHQQTLDDLQAEEDKVNTLTKAKTK 210


RESULT 9
O93498
ID   O93498      PRELIMINARY;      PRT;  1287 AA.
AC   O93498;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Myosin heavy chain (Fragment).
OS   Theragra chalcogramma.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Theragra.
OX   NCBI_TaxID=48550;
RN   [1]
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RP   SEQUENCE FROM N.A.
RC   TISSUE=SKELETAL MUSCLE;
RA   Ojima T., Kawashima N., Inoue A., Amauchi A., Togashi M., Watabe S.,
RA   Nishita K.;
RT   "Determination of Primary Structure of Heavy Meromyosin Region of
RT   Walleye Pollack Myosin Heavy Chain by cDNA Cloning.";
RL   Fisheries Sci. 0:0-0(1998).
DR   EMBL; AB017819; BAA33452.1; -.
DR   HSSP; P13538; 2MYS.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR001609; myosin_head.
DR   InterPro; IPR004009; Myosin_N.
DR   InterPro; IPR002928; Myosin_tail.
DR   InterPro; IPR000533; Tropomyosin.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF00063; myosin_head; 1.
DR   Pfam; PF02736; Myosin_N; 1.
DR   Pfam; PF01576; Myosin_tail; 1.
DR   PRINTS; PR00193; MYOSINHEAVY.
DR   PRINTS; PR00194; TROPOMYOSIN.
DR   ProDom; PD000355; myosin_head; 1.
DR   SMART; SM00015; IQ; 1.
DR   SMART; SM00242; MYSc; 1.
FT   NON_TER    1287   1287
SQ   SEQUENCE   1287 AA;  146467 MW;  BAD93CB005D6A7CD CRC64;

  Query Match             24.9%;  Score 63;  DB 13;  Length 1287;
  Best Local Similarity   45.5%;  Pred. No. 49;
  Matches   15;  Conservative    7;  Mismatches    9;  Indels    2;  Gaps    1;

Qy         21 KEDNVLVESHEKSLG--EANKADVNVLTKAKSQ 51
              ||   | |||:::|   :| :  || |||||::
Db        996 KEKKALQESHQQTLDDLQAEEDKVNTLTKAKTK 1028


RESULT 10
Q98TQ6
ID   Q98TQ6      PRELIMINARY;      PRT;  1929 AA.
AC   Q98TQ6;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Myosin heavy chain.
GN   MYOHC-A1.
OS   Notothenia coriiceps (black rockcod).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
OC   Notothenioidei; Nototheniidae; Notothenia.
OX   NCBI_TaxID=8208;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Gauvry L., Ennion S., Ettelaie C., Goldspink G.;
RT   "Characterisation of red and white muscle myosin heavy chain gene
RT   coding sequences from Antarctic and tropical fish.";
RL   Comp. Biochem. Physiol. 127:575-588(2000).
DR   EMBL; AJ243767; CAC27776.1; -.
DR   HSSP; P13538; 2MYS.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR001609; myosin_head.
DR   InterPro; IPR004009; Myosin_N.
DR   InterPro; IPR002928; Myosin_tail.
DR   Pfam; PF00612; IQ; 2.
DR   Pfam; PF00063; myosin_head; 1.
DR   Pfam; PF02736; Myosin_N; 1.
DR   Pfam; PF01576; Myosin_tail; 1.
DR   PRINTS; PR00193; MYOSINHEAVY.
DR   ProDom; PD000355; myosin_head; 1.
DR   SMART; SM00015; IQ; 1.
DR   SMART; SM00242; MYSc; 1.
SQ   SEQUENCE   1929 AA;  221167 MW;  20A78CBA19DE851B CRC64;

  Query Match             24.9%;  Score 63;  DB 13;  Length 1929;
  Best Local Similarity   45.5%;  Pred. No. 77;
  Matches   15;  Conservative    7;  Mismatches    9;  Indels    2;  Gaps    1;

Qy         21 KEDNVLVESHEKSLG--EANKADVNVLTKAKSQ 51
              ||   | |||:::|   :| :  || |||||::
Db        988 KEKKALQESHQQTLDDLQAEEDKVNTLTKAKTK 1020


RESULT 11
Q99WC5
ID   Q99WC5      PRELIMINARY;      PRT;   565 AA.
AC   Q99WC5;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   DNA polymerase III gamma and tau subunits.
GN   DNAX OR SAV0478 OR SA0436.
OS   Staphylococcus aureus (strain Mu50 / ATCC 700699), and
OS   Staphylococcus aureus (strain N315).
OC   Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC   Staphylococcus.
OX   NCBI_TaxID=158878, 158879;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   SPECIES=S.aureus (strain Mu50), and S.aureus (strain N315);
RX   MEDLINE=21311952; PubMed=11418146;
RA   Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA   Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA   Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA   Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA   Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA   Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA   Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT   "Whole genome sequencing of meticillin-resistant Staphylococcus
RT   aureus.";
RL   Lancet 357:1225-1240(2001).
DR   EMBL; AP003359; BAB56640.1; -.
DR   EMBL; AP003130; BAB41666.1; -.
DR   InterPro; IPR003593; AAA_ATPase.
DR   InterPro; IPR003959; AAA_ATPase_centr.
DR   InterPro; IPR001270; Chaprnin_clpA/B.
DR   InterPro; IPR000345; CytC_heme_bind.
DR   InterPro; IPR000463; Fatty_acid_BP.
DR   InterPro; IPR000862; RFCdomain.
DR   Pfam; PF00004; AAA; 1.
DR   PRINTS; PR00300; CLPPROTEASEA.
DR   SMART; SM00382; AAA; 1.
DR   PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR   PROSITE; PS00214; FABP; UNKNOWN_1.
KW   Complete proteome.
SQ   SEQUENCE   565 AA;  63471 MW;  F29A7F07095F02AA CRC64;

  Query Match             24.1%;  Score 61;  DB 16;  Length 565;
  Best Local Similarity   31.9%;  Pred. No. 35;
  Matches   15;  Conservative   11;  Mismatches   17;  Indels    4;  Gaps    1;

Qy          3 ALGAPLAPRDAGSQRP----RKKEDNVLVESHEKSLGEANKADVNVL 45
              | |  :||    |::|    :| ::   ::   | | :|||||: :|
Db        391 AQGVSVAPAQKSSKKPARGIQKSKNAFSMQQIAKVLDKANKADIKLL 437


RESULT 12
Q90338
ID   Q90338      PRELIMINARY;      PRT;  1092 AA.
AC   Q90338;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Myosin heavy chain (Fragment).
OS   Cyprinus carpio (Common carp).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Cyprinus.
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OX   NCBI_TaxID=7962;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=FAST MUSCLE;
RX   MEDLINE=97176447; PubMed=9023993;
RA   Imai J., Hirayama Y., Kikuchi K., Kakinuma M., Watabe S.;
RT   "cDNA cloning of myosin heavy chain isoforms from carp fast skeletal
RT   muscle and their gene expression associated with temperature
RT   acclimation.";
RL   J. Exp. Biol. 200:27-34(1997).
DR   EMBL; D50475; BAA09068.1; -.
DR   InterPro; IPR002928; Myosin_tail.
DR   InterPro; IPR000533; Tropomyosin.
DR   Pfam; PF01576; Myosin_tail; 1.
DR   PRINTS; PR00194; TROPOMYOSIN.
FT   NON_TER       1      1
SQ   SEQUENCE   1092 AA;  125885 MW;  B6BABBA3963BEEBA CRC64;

  Query Match             23.7%;  Score 60;  DB 13;  Length 1092;
  Best Local Similarity   42.4%;  Pred. No. 96;
  Matches   14;  Conservative    8;  Mismatches    9;  Indels    2;  Gaps    1;

Qy       21 KEDNVLVESHEKSLG--EANKADVNVLTKAKSQ 51
            ||   | |:|:::|   :| :  || |||||::
Db      153 KEKKALQEAHQQTLDDLQAEEDKVNTLTKAKTK 185


RESULT 13
Q9DGD5
ID   Q9DGD5      PRELIMINARY;      PRT;  1930 AA.
AC   Q9DGD5;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Myosin heavy chain.
OS   Pennahia argentata.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;
OC   Sciaenidae; Pennahia.
OX   NCBI_TaxID=118565;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=FAST MUSCLE;
RA   Yoon S., Kakinuma M., Hirayama Y., Yamamoto J., Watabe S.;
RT   "cDNA cloning and characterizaion of the complete primary structure of
RT   myosin heavy chain from white croaker fast skeletal muscle.";
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB039672; BAB12571.1; -.
DR   HSSP; P13538; 2MYS.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR001609; myosin_head.
DR   InterPro; IPR004009; Myosin_N.
DR   InterPro; IPR002928; Myosin_tail.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF00063; myosin_head; 1.
DR   Pfam; PF02736; Myosin_N; 1.
DR   Pfam; PF01576; Myosin_tail; 1.
DR   PRINTS; PR00193; MYOSINHEAVY.
DR   ProDom; PD000355; myosin_head; 1.
DR   SMART; SM00015; IQ; 1.
DR   SMART; SM00242; MYSc; 1.
DR   PROSITE; PS50096; IQ; 1.
SQ   SEQUENCE   1930 AA;  221208 MW;  C6219EB07CB4C5A1 CRC64;

  Query Match             23.7%;  Score 60;  DB 13;  Length 1930;
  Best Local Similarity   42.4%;  Pred. No. 1.8e+02;
  Matches   14;  Conservative    8;  Mismatches    9;  Indels    2;  Gaps    1;

Qy       21 KEDNVLVESHEKSLG--EANKADVNVLTKAKSQ 51
            ||   | |:|:::|   :| :  || |||||::
Db      989 KEKKALQEAHQQTLDDLQAEEDKVNTLTKAKTK 1021
```

```
RESULT 14
O42352
ID   O42352      PRELIMINARY;      PRT;  1931 AA.
AC   O42352;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Myosin heavy chain.
OS   Cyprinus carpio (Common carp).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Cyprinus.
OX   NCBI_TaxID=7962;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=FAST MUSCLE;
RX   MEDLINE=97352533; PubMed=9208928;
RA   Hirayama Y., Watabe S.;
RT   "Structural differences in the crossbridge head of temperature-
RT   associated myosin subfragment-1 isoforms from carp fast skeletal
RT   muscle.";
RL   Eur. J. Biochem. 246:380-387(1997).
DR   EMBL; D89991; BAA22068.1; -.
DR   HSSP; P13538; 2MYS.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR001609; myosin_head.
DR   InterPro; IPR004009; Myosin_N.
DR   InterPro; IPR002928; Myosin_tail.
DR   Pfam; PF00612; IQ; 2.
DR   Pfam; PF00063; myosin_head; 1.
DR   Pfam; PF02736; Myosin_N; 1.
DR   Pfam; PF01576; Myosin_tail; 1.
DR   PRINTS; PR00193; MYOSINHEAVY.
DR   ProDom; PD000355; myosin_head; 1.
DR   SMART; SM00015; IQ; 1.
DR   SMART; SM00242; MYSc; 1.
SQ   SEQUENCE   1931 AA;  221162 MW;  59466B7BD0872DDD CRC64;

  Query Match             23.7%;  Score 60;  DB 13;  Length 1931;
  Best Local Similarity   42.4%;  Pred. No. 1.8e+02;
  Matches   14;  Conservative    8;  Mismatches    9;  Indels    2;  Gaps    1;

Qy       21 KEDNVLVESHEKSLG--EANKADVNVLTKAKSQ 51
            ||   | |:|:::|   :| :  || |||||::
Db      992 KEKKALQEAHQQTLDDLQAEEDKVNTLTKAKTK 1024


RESULT 15
Q910C5
ID   Q910C5      PRELIMINARY;      PRT;  1931 AA.
AC   Q910C5;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Chick atrial myosin heavy chain.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=HEART;
RA   Oana S., Machida S., Furutani Y., Hiratsuka E., Momma K., Takao A.,
RA   Matsuoka R.;
RT   "Characterization and expression pattern of atrial myosin heavy chain
RT   gene in developing chick.";
RL   Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB004801; BAB47399.1; -.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR001609; myosin_head.
DR   InterPro; IPR004009; Myosin_N.
```

```
DR   InterPro; IPR002928; Myosin_tail.
DR   InterPro; IPR002017; Spectrin.
DR   Pfam; PF00612; IQ; 2.
DR   Pfam; PF00063; myosin_head; 1.
DR   Pfam; PF02736; Myosin_N; 1.
DR   Pfam; PF01576; Myosin_tail; 1.
DR   ProDom; PD000355; myosin_head; 1.
DR   SMART; SM00015; IQ; 1.
DR   PROSITE; PS50096; IQ; 1.
SQ   SEQUENCE   1931 AA;  221802 MW;  EB57D688E03397D2 CRC64;

  Query Match             23.7%;  Score 60;  DB 13;  Length 1931;
  Best Local Similarity   42.4%;  Pred. No. 1.8e+02;
  Matches   14;  Conservative    7;  Mismatches   10;  Indels    2;  Gaps    1;

Qy      21 KEDNVLVESHEKSLG--EANKADVNVLTKAKSQ 51
           ||  :| |||:::|   :| :  || | ||| :
Db     989 KEKKILQESHQQALDDLQAEEDKVNTLAKAKGK 1021


Search completed: March 13, 2003, 15:01:52
Job time : 21.791 secs
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                     GenCore version 5.1.4_p5_4578
             Copyright (c) 1993 - 2003  Compugen Ltd.

OM protein - protein search, using sw model

Run on:         March 13, 2003, 14:52:29 ; Search time 39.6418 Seconds
                                          (without alignments)
                                          278.993 Million cell updates/sec

Title:          US-09-636-530-2
Perfect score:  422
Sequence:       1 VSEIQLMHNLGKHLNSMERV..........KSLGEANKADVNVLTKAKSQ 83

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters:      908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      A_Geneseq_101002:*
                1:  /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
                2:  /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
                3:  /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
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                8:  /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
                9:  /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
                10:  /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
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                13:  /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
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                16:  /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:*
                17:  /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:*
                18:  /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*
                19:  /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:*
                20:  /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
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                23:  /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                     SUMMARIES
                  %
Result          Query
  No.   Score   Match Length DB  ID                    Description
 -------------------------------------------------------------------------------
    1    422   100.0     84  21  AAB07464              Amino acid sequenc
    2    418    99.1     82  21  AAB07465              Amino acid sequenc
    3    417    98.8     84  13  AAR23790              Parathyroid hormon
    4    417    98.8     84  13  AAR25571              Human PTH encoded
    5    417    98.8     84  14  AAR42067              Human parathyroid
    6    417    98.8     84  17  AAW29420              Human parathyroid
    7    417    98.8     84  17  AAR98954              Target peptide (PT
    8    417    98.8     84  18  AAW25687              Human parathyroid
    9    417    98.8     84  20  AAY02577              Human parathyroid
   10    417    98.8     84  22  AAB91082              Parathyroid hormon
   11    417    98.8     84  23  AAE23726              Human parathyroid
   12    417    98.8     84  23  ABB08594              Human parathyroid
   13    417    98.8     84  23  AAE18392              Human PTH peptide
   14    417    98.8     84  23  AAE14316              Salmon calcitonin
   15    417    98.8     84  23  AAU73022              Parathyroid hormon
   16    417    98.8    115   5  AAP40251             Protein sequence i
   17    417    98.8    115   9  AAP80305             Sequence of human
   18    417    98.8    115   9  AAP80275             Sequence of human
   19    417    98.8    115  16  AAR75693              Human prepro-PTH.
   20    414    98.1     84  13  AAR28846              Oxidation resistan
   21    414    98.1     84  13  AAR28848              Oxidation resistan
   22    414    98.1     84  14  AAR30857              Leu18 hPTH mutein.
   23    413    97.9     84  14  AAR42068              Stability-enhanced
   24    412    97.6     84  14  AAR30856              Cys35 hPTH mutein.
   25    412    97.6     84  14  AAR42070              Stability-enhanced
   26    412    97.6     84  17  AAW99448              Human parathyroid
   27    411    97.4     84  13  AAR28845              Oxidation resistan
   28    411    97.4     84  13  AAR28847              Oxidation resistan
   29    411    97.4     84  13  AAR29562              Oxidation resistan
   30    411    97.4     84  14  AAR42071              Stability-enhanced
   31    411    97.4     84  15  AAR49692              Sequence of varian
   32    411    97.4     84  15  AAR49693              Sequence of varian
   33    411    97.4     84  15  AAR49694              Sequence of varian
   34    410    97.2     84  13  AAR29564              Oxidation resistan
   35    410    97.2     84  13  AAR29565              Oxidation resistan
   36    410    97.2     84  14  AAR42069              Stability-enhanced
   37    410    97.2     84  15  AAR49696              Sequence of varian
   38    409    96.9     81  14  AAR30854              hPTH mutein lackin
   39    409    96.9     84  13  AAR21155              Human parathyroid
   40    409    96.9     84  13  AAR23238              Human parathyroid
   41    409    96.9     84  13  AAR23239              Human parathyroid
   42    409    96.9     84  13  AAR23244              Human parathyroid
   43    409    96.9     84  13  AAR21250              Human parathyroid
   44    409    96.9     84  13  AAR21251              Human parathyroid
   45    409    96.9     84  13  AAR21256              Human parathyroid


                                   ALIGNMENTS


RESULT 1
AAB07464
ID   AAB07464 standard; protein; 84 AA.
XX
AC   AAB07464;
XX
DT   20-OCT-2000  (first entry)
XX
DE   Amino acid sequence of human parathyroid hormone.
XX
KW   Human; parathyroid hormone; PTH; hyperparathyroidism; bone disease.
XX
OS   Homo sapiens.
XX
PN   WO200042437-A1.
XX
PD   20-JUL-2000.
XX
PF   13-JAN-2000; 2000WO-US00855.
XX
PR   14-JAN-1999;   99US-0231422.
PR   26-JUN-1999;   99US-0344639.
XX
PA   (SCAN-) SCANTIBODIES LAB INC.
XX
DR   WPI; 2000-476147/41.
XX
PT   Differentiating between normal parathyroid function and
PT   hyperparathyroidism comprises determining and comparing whole
PT   parathyroid hormone, parathyroid hormone inhibitory peptide fragment
PT   and/or total parathyroid hormone levels -
XX
PS   Disclosure; Fig 1; 46pp; English.
```

```
XX
CC   The present sequence represents a human parathyroid hormone (PTH).
CC   Fragments of PTH function as PTH antagonists. The specification
CC   describes a method for differentiating between a person having
CC   substantially normal parathyroid function and having hyperparathyroidism.
CC   The method comprises determining and comparing at least two of the
CC   following parameters: whole parathyroid hormone level, parathyroid
CC   hormone inhibitory peptide fragment level and total parathyroid hormone
CC   level. The method is used for monitoring (treatments of) parathyroid
CC   related bone disease and the effects of therapeutic treatment for
CC   hyperparathyroidism.
XX
SQ   Sequence   84 AA;

  Query Match             100.0%;  Score 422;  DB 21;  Length 84;
  Best Local Similarity   100.0%;  Pred. No. 5e-42;
  Matches   83;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 61

Qy       61 SHEKSLGEANKADVNVLTKAKSQ 83
            |||||||||||||||||||||||
Db       62 SHEKSLGEANKADVNVLTKAKSQ 84


RESULT 2
AAB07465
ID   AAB07465 standard; protein; 82 AA.
XX
AC   AAB07465;
XX
DT   20-OCT-2000  (first entry)
XX
DE   Amino acid sequence of human parathyroid hormone antagonist.
XX
KW   Human; parathyroid hormone; PTH; hyperparathyroidism; bone disease.
XX
OS   Homo sapiens.
XX
PN   WO200042437-A1.
XX
PD   20-JUL-2000.
XX
PF   13-JAN-2000; 2000WO-US00855.
XX
PR   14-JAN-1999;   99US-0231422.
PR   26-JUN-1999;   99US-0344639.
XX
PA   (SCAN-) SCANTIBODIES LAB INC.
XX
DR   WPI; 2000-476147/41.
XX
PT   Differentiating between normal parathyroid function and
PT   hyperparathyroidism comprises determining and comparing whole
PT   parathyroid hormone, parathyroid hormone inhibitory peptide fragment
PT   and/or total parathyroid hormone levels -
XX
PS   Disclosure; Page 42-43; 46pp; English.
XX
CC   The present sequence represents a fragment of human parathyroid
CC   hormone (PTH), comprising residues 3-84, which functions as a PTH
CC   antagonist. The specification describes a method for differentiating
CC   between a person having substantially normal parathyroid function
CC   and having hyperparathyroidism. The method comprises determining and
CC   comparing at least two of the following parameters: whole parathyroid
CC   hormone level, parathyroid hormone inhibitory peptide fragment level
CC   and total parathyroid hormone level. The method is used for monitoring
CC   (treatments of) parathyroid related bone disease and the effects of
CC   therapeutic treatment for hyperparathyroidism.
XX
SQ   Sequence   82 AA;

  Query Match              99.1%;  Score 418;  DB 21;  Length 82;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-41;
  Matches   82;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        2 SEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVES 61
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 SEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVES 60

Qy       62 HEKSLGEANKADVNVLTKAKSQ 83
            ||||||||||||||||||||||
Db       61 HEKSLGEANKADVNVLTKAKSQ 82


RESULT 3
AAR23790
ID   AAR23790 standard; Protein; 84 AA.
XX
AC   AAR23790;
XX
DT   03-NOV-1992  (first entry)
XX
DE   Parathyroid hormone gene product.
XX
KW   hPTH; hypoparathyroidism; osteoporosis.
XX
OS   Synthetic.
XX
PN   EP483509-A.
XX
PD   06-MAY-1992.
XX
PF   25-SEP-1991;   91EP-0116281.
XX
PR   28-SEP-1990;   90JP-0257491.
PR   20-MAR-1991;   91JP-0056434.
XX
PA   (TAKE ) TAKEDA CHEM IND LTD.
XX
PI   Fukuda T,  Oshika Y,  Yamada T;
XX
DR   WPI; 1992-152248/19.
DR   N-PSDB; AAQ24478.
XX
PT   Synthetic gene encoding human parathyroid hormone - formed by
PT   ligating oligo-nucleotide(s) and expressed at high yield in E
PT   coli
XX
PS   Disclosure; Page 21; 33pp; English.
XX
CC   The human parathyroid hormone (hPTH) sequence given is the product of
CC   a synthetic gene which corresponds to the amino acid sequence of hPTH.
CC   The DNA sequence was produced by enzymatically ligating
CC   oligodeoxynucleotides.  hPTH is an important regulator of calcium
CC   metabolism and has clinical applicns. to diseases such as
CC   hypoparathyroidism and osteoporosis.  This hPTH  can be used as a
CC   therapeutic agent or to study the biological role of hPTH in vivo.
XX
SQ   Sequence   84 AA;

  Query Match              98.8%;  Score 417;  DB 13;  Length 84;
  Best Local Similarity    98.8%;  Pred. No. 1.9e-41;
  Matches   82;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 61

Qy       61 SHEKSLGEANKADVNVLTKAKSQ 83
            |||||||||:|||||||||||||
Db       62 SHEKSLGEADKADVNVLTKAKSQ 84
```

```
RESULT 4
AAR25571
ID   AAR25571 standard; Protein; 84 AA.
XX
AC   AAR25571;
XX
DT   13-JAN-1993  (first entry)
XX
DE   Human PTH encoded by pX.
XX
KW   Parathyroid; hormone; osteoporosis; psoriasis; oxidation;
KW   resistance.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 8
FT                   /note= "see CC"
FT   Misc-difference 18
FT                   /note= "see CC"
XX
PN   WO9211286-A.
XX
PD   09-JUL-1992.
XX
PF   18-DEC-1991;   91WO-CA00451.
XX
PR   21-DEC-1990;   90US-0630969.
PR   13-DEC-1991;   91US-0806271.
XX
PA   (ALLE-) ALLELIX BIOPHARMACEUTICALS INC.
PA   (GLAX ) GLAXO CANADA INC.
XX
PI   Bozatto RP,  Kronis KA;
XX
DR   WPI; 1992-250028/30.
DR   N-PSDB; AAQ26498.
XX
PT   New oxidn. resistant variants of parathyroid hormone - used for
PT   treating osteoporosis, psoriasis and cardiovascular disorders
XX
PS   Disclosure; Fig 1; 40pp; English.
XX
CC   Variants of PTH exhibiting PTH activity and reduced sensitivity
CC   to oxidation are obtained by replacing at least one Met residue in
CC   PTH (positions 8 and 18) with a genetically encoded amino acid,
CC   other than Met and Cys.
CC   The Met amino acids are indicated in the Features Table.
CC   The variant may be obtd. using recombinant technique, and may be
CC   used for treating osteoporosis, other bone-related disorders,
CC   psoriasis and cardiovascular disorders.
CC   Human PTH refers to the mature form of the hormone, which consists
CC   of 84 amino acids arranged in the sequence reported by Kimura et al,
CC   1983, Biochem. Biophys. Res. Comm., 114(2):493.
CC   Examples of variants are given in AAR28845-48 and AAR29561-69.
XX
SQ   Sequence   84 AA;

  Query Match             98.8%;  Score 417;  DB 13;  Length 84;
  Best Local Similarity   98.8%;  Pred. No. 1.9e-41;
  Matches   82;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 61

Qy         61 SHEKSLGEANKADVNVLTKAKSQ 83
              |||||||||:|||||||||||||
Db         62 SHEKSLGEADKADVNVLTKAKSQ 84


RESULT 5
AAR42067
ID   AAR42067 standard; Protein; 84 AA.
XX
AC   AAR42067;
XX
DT   05-MAY-1994  (first entry)
XX
DE   Human parathyroid hormone.
XX
KW   PTH; hPTH; stability-enhanced; mutant; resistance; proteolytic;
KW   enzymes; osteoporosis; bone-related disorders.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          25..27
FT                   /note= "ArgLysLys which may be mutated"
XX
PN   WO9320203-A.
XX
PD   14-OCT-1993.
XX
PF   31-MAR-1993;   93WO-CA00136.
XX
PR   03-APR-1992;   92US-0863014.
XX
PA   (ALLE-) ALLELIX BIOPHARMACEUTICALS INC.
PA   (GLAX ) GLAXO CANADA INC.
XX
PI   Bozzato RP,  Kronis KA;
XX
DR   WPI; 1993-336911/42.
DR   N-PSDB; AAQ49955.
XX
PT   New parathyroid hormone variants - having aminoacid replacements
PT   at positions 25 to 27 to enhance resistance to proteolytic
PT   enzymes
XX
PS   Disclosure; Fig 2; 44pp; English.
XX
CC   The sequence is that of human parathyroid hormone (hPTH) which
CC   may be mutated in the region Arg25Lys26Lys27 to provide variants
CC   with enhanced stability in the presence of proteolytic enzymes
CC   such as trypsin.
XX
SQ   Sequence   84 AA;

  Query Match             98.8%;  Score 417;  DB 14;  Length 84;
  Best Local Similarity   98.8%;  Pred. No. 1.9e-41;
  Matches   82;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 61

Qy         61 SHEKSLGEANKADVNVLTKAKSQ 83
              |||||||||:|||||||||||||
Db         62 SHEKSLGEADKADVNVLTKAKSQ 84


RESULT 6
AAW29420
ID   AAW29420 standard; protein; 84 AA.
XX
AC   AAW29420;
XX
DT   24-FEB-1998  (first entry)
XX
DE   Human parathyroid hormone.
XX
KW   Parathyroid hormone; PTH; osteoporosis; inhalation; pulmonary;
KW   bone formation.
XX
OS   Homo sapiens.
```

```
XX
PN   WO9619206-A1.
XX
PD   27-JUN-1996.
XX
PF   08-DEC-1995;   95WO-SE01475.
XX
PR   12-JUL-1995;   95SE-0002576.
PR   22-DEC-1994;   94SE-0004449.
XX
PA   (ASTR ) ASTRA AB.
XX
PI   Backstrom K,  Wallmark B;
XX
DR   WPI; 1996-309285/31.
XX
PT   Composition for administration by inhalation to treat osteoporosis
PT   and stimulate bone formation - comprises parathyroid hormone in form
PT   of dry powder mainly of particle size below 10 microns
XX
PS   Claim 9; Pages 15-16; 25pp; English.
XX
CC   The present sequence represents human parathyroid hormone which is used
CC   in a new therapeutic preparation for the treatment of osteoporosis.
CC   The active substance is in the form of a dry powder suitable for
CC   inhalation, in which at least 50% of the dry powder consists of particles
CC   of up to 10 microns in diameter or agglomerates of such particles.
CC   Pulmonary administration of the parathyroid hormone is effective in the
CC   stimulation of bone formation.
XX
SQ   Sequence   84 AA;

  Query Match             98.8%;  Score 417;  DB 17;  Length 84;
  Best Local Similarity   98.8%;  Pred. No. 1.9e-41;
  Matches   82;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 61

Qy      61 SHEKSLGEANKADVNVLTKAKSQ 83
           |||||||||:|||||||||||||
Db      62 SHEKSLGEADKADVNVLTKAKSQ 84


RESULT 7
AAR98954
ID   AAR98954 standard; peptide; 84 AA.
XX
AC   AAR98954;
XX
DT   15-JAN-1997  (first entry)
XX
DE   Target peptide (PTH(1-84)) used in fusion protein construct.
XX
KW   Fusion protein construct; isolation; purification;
KW   growth hormone releasing factor; glucagon-like peptide 1;
KW   parathyroid hormone; inclusion body; carbonic anhydrase.
XX
OS   Synthetic.
XX
PN   WO9617942-A1.
XX
PD   13-JUN-1996.
XX
PF   07-DEC-1995;   95WO-US15800.
XX
PR   07-DEC-1994;   94US-0350530.
XX
PA   (BION-) BIONEBRASKA INC.
XX
PI   De LA MOTTE RS,  Henriksen DB,  Holmquist B,  Manning SD;
PI   Partridge BE, Stout JS,  Wagner FW;
```

```
XX
DR   WPI; 1996-287186/29.
XX
PT   Isolation and purificn of peptide(s) from fusion protein constructs
PT   - which include a carbonic anhydrase and a variable fused
PT   polypeptide
XX
PS   Claim 58; Page 49; 67pp; English.
XX
CC   A new method for the isolation and/or purification of a recombinant
CC   peptide employs a fusion protein construct (FPC) comprising a
CC   carbonic anhydrase and a variable fused polypeptide containing a
CC   target peptide.  The method comprises precipitating either the FPC or
CC   a fragment of the FPC including the carbonic anhydrase.  An
CC   alternative method of producing the peptide comprises expressing the
CC   FPC as part of an inclusion body.  The target peptides of the FPC are
CC   derived from growth hormone releasing factor (GRF), glucagon-like
CC   peptide 1 (GLP1) or parathyroid hormone (PTH).  This sequence
CC   corresponds to amino acids 1-84 of PTH.
XX
SQ   Sequence   84 AA;

  Query Match             98.8%;  Score 417;  DB 17;  Length 84;
  Best Local Similarity   98.8%;  Pred. No. 1.9e-41;
  Matches   82;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 61

Qy      61 SHEKSLGEANKADVNVLTKAKSQ 83
           |||||||||:|||||||||||||
Db      62 SHEKSLGEADKADVNVLTKAKSQ 84


RESULT 8
AAW25687
ID   AAW25687 standard; Peptide; 84 AA.
XX
AC   AAW25687;
XX
DT   14-APR-1998  (first entry)
XX
DE   Human parathyroid hormone peptide hPTH (residues 1-84).
XX
KW   Kex2 protease; derivative; cleave; yeast; enzyme; chimeric protein;
KW   human;  parathyroid hormone peptide; hPTH.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Cleavage-site   43..44
FT                   /note= "cleaved by Kex2 protease"
FT   Cleavage-site   51..52
FT                   /note= "cleaved by Kex2 protease"
XX
PN   EP794254-A2.
XX
PD   10-SEP-1997.
XX
PF   04-MAR-1997;   97EP-0301429.
XX
PR   16-DEC-1996;   96JP-0352580.
PR   04-MAR-1996;   96JP-0073217.
XX
PA   (SUNR ) SUNTORY LTD.
XX
PI   Magota K,  Masuda T,  Suzuki Y,  Yabuta M;
XX
DR   WPI; 1997-437479/41.
XX
PT   Secreted forms of Kex2 protease - useful for cleaving chimeric
PT   proteins
```

```
XX
PS   Disclosure; Page 25; 82pp; English.
XX
CC   This is the human parathyroid hormone peptide hPTH (residues 1-84). This
CC   is used in the construction of a chimeric protein betaGal-139S(FM)PPH84.
CC   The enzyme Kex2 protease can be used for excision of a desired protein
CC   from a chimeric protein comprising the desired protein and an Arg-Arg,
CC   Lys-Arg or Pro-Arg sequence adjacent to the N terminus of the desired
CC   protein. It can be specifically used for cleaving this human parathyroid
CC   hormone peptide hPTH(1-84) or peptide hPTH(1-34) from chimeric proteins
CC   such as the beta Gal-139S(FM)PPH84 or CATPH34. Derivatives of Kex2
CC   protease, and especially Kex2-660 can also cleave such chimeric proteins
CC   with high specificity and efficiency even in the absence of urea.
XX
SQ   Sequence   84 AA;

  Query Match             98.8%;  Score 417;  DB 18;  Length 84;
  Best Local Similarity   98.8%;  Pred. No. 1.9e-41;
  Matches   82;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 61

Qy         61 SHEKSLGEANKADVNVLTKAKSQ 83
              |||||||||:|||||||||||||
Db         62 SHEKSLGEADKADVNVLTKAKSQ 84

RESULT 9
AAY02577
ID   AAY02577 standard; protein; 84 AA.
XX
AC   AAY02577;
XX
DT   16-JUL-1999  (first entry)
XX
DE   Human parathyroid hormone (hPTH) protein.
XX
KW   Human parathyroid hormone; hPTH; bone mass;
KW   3-(substituted phenoxy)benzo(b)thiophene compound;
KW   bone loss treatment; osteoporosis.
XX
OS   Homo sapiens.
XX
PN   WO9918945-A1.
XX
PD   22-APR-1999.
XX
PF   05-OCT-1998;   98WO-US20848.
XX
PR   14-OCT-1997;   97US-0061800.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Sato M;
XX
DR   WPI; 1999-287871/24.
XX
PT   Method of building bone mass by co-administration of a parathyroid
PT   hormone with a 3-(substituted phenoxy)benzo(b)thiophene compound
XX
PS   Claim 5; Page 38; 48pp; English.
XX
CC   The present sequence represents human parathyroid hormone (hPTH). It,
CC   and its fragments, are used in the method of the invention. The
CC   specification describes a method for building bone mass, comprising
CC   coadministration of a parathyroid hormone with a 3-(substituted
CC   phenoxy)benzo(b)thiophene compound. The method is used for treatment
CC   of bone loss, e.g. in osteoporosis.
XX
SQ   Sequence   84 AA;
```

```
  Query Match             98.8%;  Score 417;  DB 20;  Length 84;
  Best Local Similarity   98.8%;  Pred. No. 1.9e-41;
  Matches   82;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 61

Qy         61 SHEKSLGEANKADVNVLTKAKSQ 83
              |||||||||:|||||||||||||
Db         62 SHEKSLGEADKADVNVLTKAKSQ 84

RESULT 10
AAB91082
ID   AAB91082 standard; Peptide; 84 AA.
XX
AC   AAB91082;
XX
DT   22-JUN-2001  (first entry)
XX
DE   Parathyroid hormone (PTH) related peptide SEQ ID NO:256.
XX
KW   Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW   blood component; modification; succinimidyl; maleimido group; amino;
KW   hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200069900-A2.
XX
PD   23-NOV-2000.
XX
PF   17-MAY-2000; 2000WO-US13576.
XX
PR   17-MAY-1999;   99US-0134406.
PR   10-SEP-1999;   99US-0153406.
PR   15-OCT-1999;   99US-0159783.
XX
PA   (CONJ-) CONJUCHEM INC.
XX
PI   Bridon DP,  Ezrin AM,  Milner PG,  Holmes DL,  Thibaudeau K;
XX
DR   WPI; 2001-112059/12.
XX
PT   Modifying and attaching therapeutic peptides to albumin prevents
PT   peptidase degradation, useful for increasing length of in vivo activity
PT   -
XX
PS   Disclosure; Page 274-275; 733pp; English.
XX
CC   The present invention describes a modified therapeutic peptide (I)
CC   comprising a therapeutically active amino acid region (III) and a
CC   reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC   a less therapeutically active amino acid region (IV), which covalently
CC   bonds with amino/hydroxyl/thiol groups on blood components to form a
CC   peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC   (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC   factors and neurotransmitters, to protect them from peptidase activity
CC   in vivo for the treatment of various disorders. Endogenous therapeutic
CC   peptides are not suitable as drug candidates as they require frequent
CC   administration due to rapid degradation by peptidases in the body.
CC   Modifying and attaching therapeutic peptides to albumin prevents or
CC   reduces the action of peptidases to increase length of activity (half
CC   life) and specificity as bonding to large molecules decreases
CC   intracellular uptake and interference with physiological processes.
CC   AAB90829 to AAB92441 represent peptides which can be used in the
CC   exemplification of the present invention.
XX
SQ   Sequence   84 AA;

  Query Match             98.8%;  Score 417;  DB 22;  Length 84;
```

```
  Best Local Similarity   98.8%;  Pred. No. 1.9e-41;
  Matches   82;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 61

Qy         61 SHEKSLGEANKADVNVLTKAKSQ 83
              |||||||||:|||||||||||||
Db         62 SHEKSLGEADKADVNVLTKAKSQ 84


RESULT 11
AAE23726
ID   AAE23726 standard; peptide; 84 AA.
XX
AC   AAE23726;
XX
DT   10-SEP-2002  (first entry)
XX
DE   Human parathyroid hormone (hPTH) peptide (1-84).
XX
KW   Human parathyroid hormone; hPTH; PTH-related peptide; PTHrP; eczema;
KW   hyperproliferative skin disorder; psoriasis; ichthyosis; skin cancer;
KW   acne; actinic keratosis; alopecia; gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO200228420-A2.
XX
PD   11-APR-2002.
XX
PF   05-OCT-2001; 2001WO-US31082.
XX
PR   06-OCT-2000; 2000US-238134P.
XX
PA   (HOLI/) HOLICK M F.
XX
PI   Holick MF;
XX
DR   WPI; 2002-452304/48.
DR   N-PSDB; AAD37995.
XX
PT   Regulating mammalian skin or hair cell proliferation and
PT   differentiation by administering nucleic acids encoding peptides
PT   derived from N-terminal region of human parathyroid hormone (hPTH) or
PT   hPTH-related protein  -
XX
PS   Claim 5; Fig 18; 56pp; English.
XX
CC   The invention relates to a method for regulating proliferation or
CC   enhancing differentiation of mammalian skin or hair cell. The method
CC   involves administering nucleic acids encoding peptides derived from
CC   N-terminal region of human parathyroid hormone (hPTH) or hPTH-related
CC   peptide (PTHrP). The method is used for inhibiting hyperproliferative
CC   skin disorders such as psoriasis, ichthyosis, eczema, acne, actinic
CC   keratosis, skin cancer, for inhibiting hair growth or preventing hair
CC   regrowth. It is useful for stimulating cell growth, rejuvenating aged
CC   skin, preventing skin wrinkles, treating skin wrinkles, enhancing wound
CC   healing, stimulating hair growth, maintaining hair growth, treating or
CC   preventing female or male pattern baldness, for treating chemotherapy
CC   induced alopecia and also for stimulating epidermal cell growth or
CC   hair follicle cell growth. The method is also used in gene therapy.
CC   The present sequence is hPTH peptide.
XX
SQ   Sequence   84 AA;

  Query Match             98.8%;  Score 417;  DB 23;  Length 84;
  Best Local Similarity   98.8%;  Pred. No. 1.9e-41;
  Matches   82;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 61

Qy         61 SHEKSLGEANKADVNVLTKAKSQ 83
              |||||||||:|||||||||||||
Db         62 SHEKSLGEADKADVNVLTKAKSQ 84


RESULT 12
ABB08594
ID   ABB08594 standard; protein; 84 AA.
XX
AC   ABB08594;
XX
DT   23-MAY-2002  (first entry)
XX
DE   Human parathyroid hormone.
XX
KW   Human; parathyroid hormone; hPTH; osteopathic.
XX
OS   Homo sapiens.
XX
PN   WO200202136-A1.
XX
PD   10-JAN-2002.
XX
PF   29-JUN-2001; 2001WO-JP05674.
XX
PR   30-JUN-2000; 2000JP-0237717.
PR   30-JUN-2000; 2000JP-0237718.
XX
PA   (SUNR ) SUNTORY LTD.
XX
PI   Minamitake Y,  Ono T,  Kawanishi K,  Suzuki Y;
XX
DR   WPI; 2002-147974/19.
XX
PT   Drug compositions for nasal administration comprising human parathyroid
PT   hormone peptide or its derivative and acetic acid, is applicable for
PT   long-term therapy of osteoporosis  -
XX
PS   Claim 3; Page 64; 67pp; Japanese.
XX
CC   This invention relates to components comprising of human parathyroid
CC   hormone peptide (hPTH) and less than their stoichiometric equivalent
CC   of acetic acid. The compositions are applicable for long-term therapy
CC   of osteoporosis. The present sequence represents human parathyroid
CC   hormone.
XX
SQ   Sequence   84 AA;

  Query Match             98.8%;  Score 417;  DB 23;  Length 84;
  Best Local Similarity   98.8%;  Pred. No. 1.9e-41;
  Matches   82;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 61

Qy         61 SHEKSLGEANKADVNVLTKAKSQ 83
              |||||||||:|||||||||||||
Db         62 SHEKSLGEADKADVNVLTKAKSQ 84


RESULT 13
AAE18392
ID   AAE18392 standard; peptide; 84 AA.
XX
AC   AAE18392;
XX
DT   07-MAY-2002  (first entry)
XX
DE   Human PTH peptide #5.
XX
```

```
KW   Human; cell proliferation; cell differentiation; parathyroid hormone;
KW   PTH; parathyroid related peptide; hyperproliferative skin disorder;
KW   psoriasis; ichthyosis; actinic keratosis; alopecia; skin cell growth;
KW   hair growth; wrinkle; wound healing; chemotherapy; skin cancer; PTHrP.
XX
OS   Homo sapiens.
XX
PN   WO200198348-A2.
XX
PD   27-DEC-2001.
XX
PF   20-JUN-2001; 2001WO-US19650.
XX
PR   22-JUN-2000; 2000US-213247P.
XX
PA   (HOLI/) HOLICK M F.
XX
PI   Holick MF;
XX
DR   WPI; 2002-171552/22.
XX
PT   Modulating proliferation or differentiation of mammalian skin or hair
PT   cell for treating hyperproliferative diseases, comprises topical
PT   administration of liposome encapsulated-peptide identical to
PT   parathyroid hormone  -
XX
PS   Disclosure; Page 10; 58pp; English.
XX
CC   The invention relates to a method of modulating proliferation or
CC   differentiation of mammalian skin or hair cell. The method involves
CC   topical administration of a liposome encapsulated-peptide, its salt
CC   or derivative, identical to parathyroid hormone (PTH) or parathyroid
CC   related peptide (PTHrP). Method of the invention is useful for
CC   inhibiting hyperproliferative skin disorders e.g. psoriasis,
CC   ichthyosis, actinic keratosis, skin cancer, inhibiting hair growth or
CC   preventing hair regrowth. It is also useful for stimulating skin cell
CC   growth, rejuvenating aged skin, preventing and treating skin wrinkles,
CC   enhancing wound healing, stimulating hair growth, maintaining hair
CC   growth, treating or preventing female or male pattern baldness,
CC   treating chemotherapy induced alopecia and for stimulating epidermal
CC   cell growth and hair follicle cell growth. The present sequence is
CC   human PTH peptide used in the method of the invention.
XX
SQ   Sequence   84 AA;

  Query Match             98.8%;  Score 417;  DB 23;  Length 84;
  Best Local Similarity   98.8%;  Pred. No. 1.9e-41;
  Matches   82;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 61

Qy       61 SHEKSLGEANKADVNVLTKAKSQ 83
              |||||||||:|||||||||||||
Db       62 SHEKSLGEADKADVNVLTKAKSQ 84


RESULT 14
AAE14316
ID   AAE14316 standard; Protein; 84 AA.
XX
AC   AAE14316;
XX
DT   07-MAR-2002  (first entry)
XX
DE   Salmon calcitonin (CT) receptor modulating domain.
XX
KW   Calcitonin; CT; CT receptor; Fc domain; therapy; osteoporosis;
KW   osteopathic; salmon.
XX
OS   Oncorhynchus sp.
XX
PN   WO200183526-A2.
XX
PD   08-NOV-2001.
XX
PF   03-MAY-2001; 2001WO-US14320.
XX
PR   03-MAY-2000; 2000US-201511P.
PR   02-MAY-2001; 2001US-0847712.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Liu C,  Marshall WS,  Reynolds A;
XX
DR   WPI; 2002-034503/04.
XX
PT   Compositions comprising Calcitonin receptor modulator domains, useful
PT   for treating osteoporosis -
XX
PS   Claim 14; Page 17; 64pp; English.
XX
CC   The invention relates to therapeutic agents that modulate the
CC   activity of calcitonin (CT) receptor. Modulators of CT receptor
CC   comprise a CT receptor modulating domain and a vehicle such as a
CC   polymer or an Fc domain, where the vehicle is covalently attached
CC   to the CT receptor modulating domain. The compositions comprising
CC   CT receptor modulating domains are used to treat osteoporosis.
CC   The present sequence is salmon calcitonin receptor modulating domain.
XX
SQ   Sequence   84 AA;

  Query Match             98.8%;  Score 417;  DB 23;  Length 84;
  Best Local Similarity   98.8%;  Pred. No. 1.9e-41;
  Matches   82;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 61

Qy       61 SHEKSLGEANKADVNVLTKAKSQ 83
              |||||||||:|||||||||||||
Db       62 SHEKSLGEADKADVNVLTKAKSQ 84


RESULT 15
AAU73022
ID   AAU73022 standard; Peptide; 84 AA.
XX
AC   AAU73022;
XX
DT   12-MAR-2002  (first entry)
XX
DE   Parathyroid hormone PTH/PTHrP modulating domain #4.
XX
KW   Human; parathyroid hormone; PTH; parathyroid hormone-related protein;
KW   PTHrP; bone resorption inhibitor; osteoprotegrin; OPG; OPG-L antibody;
KW   calcitonin; bisphosphonate; oestrogen; oestrogen receptor; tibolone;
KW   osteopenia; hyperthyroidism; hypercalcaemia; tumour metastasis; bone;
KW   breast cancer; prostate cancer; cachexia; anorexia; osteoporosis;
KW   Paget's disease; osteomyelitis; osteonecrosis; bone cell death;
KW   Gaucher's disease; sickle cell anaemia; systemic lupus erythematosus;
KW   rheumatoid arthritis; periodontal disease; alopecia; fracture repair;
KW   immunoglobulin G; IgG.
XX
OS   Homo sapiens.
XX
PN   WO200181415-A2.
XX
PD   01-NOV-2001.
XX
PF   27-APR-2001; 2001WO-US13528.
XX
PR   27-APR-2000; 2000US-200053P.
PR   28-JUN-2000; 2000US-214860P.
```

```
PR   06-FEB-2001; 2001US-266673P.
PR   26-APR-2001; 2001US-0843221.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Kostenuik P,  Liu C,  Lacey DL;
XX
DR   WPI; 2002-066435/09.
XX
PT   Composition, useful for treating osteopenia, comprises parathyroid
PT   hormone and parathyroid hormone-related protein receptor modulators -
XX
PS   Disclosure; Page 25; 107pp; English.
XX
CC   The invention relates to a composition (I) comprising modulators of
CC   parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHrP)
CC   which comprise a PTH/PTHrP modulating domain and a vehicle. (I)
CC   comprising PTH agonist optionally with a bone resorption inhibitor, such
CC   as osteoprotegrin (OPG), OPG-L antibody, calcitonin, bisphosphonates,
CC   oestrogens, oestrogen receptor modulators and tibolone is useful for
CC   treating osteopenia. (I) is useful for therapeutic and prophylactic
CC   purposes. Antagonists of PTH receptor are useful in treating primary and
CC   secondary hyperthyroidism, hypercalcaemia, tumour metastases,
CC   particularly breast and prostate cancer, cachexia and anorexia,
CC   osteopenia, including various forms of osteoporosis, Paget's disease of
CC   bone, osteomyelitis, osteonecrosis or bone cell death, associated with
CC   traumatic injury or nontraumatic necrosis associated with Gaucher's
CC   disease, sickle cell anaemia, systemic lupus erythematosus, rheumatoid
CC   arthritis, periodontal disease and alopecia. PTH receptor agonists are
CC   useful as therapeutic agents in conditions including fracture repair
CC   (including healing of non-union fractures), osteopenia, including various
CC   forms of osteoporosis. AAU73018-AAU73181 represent parathyroid hormone
CC   and parathyroid hormone related protein (PTH/PTHrP) modulators and
CC   related amino acid sequences of the invention.
XX
SQ   Sequence   84 AA;

  Query Match             98.8%;  Score 417;  DB 23;  Length 84;
  Best Local Similarity   98.8%;  Pred. No. 1.9e-41;
  Matches   82;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
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Db          2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 61

Qy         61 SHEKSLGEANKADVNVLTKAKSQ 83
              |||||||||:|||||||||||||
Db         62 SHEKSLGEADKADVNVLTKAKSQ 84


Search completed: March 13, 2003, 15:00:25
Job time : 40.6418 secs
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                    GenCore version 5.1.4_p5_4578
             Copyright (c) 1993 - 2003  Compugen Ltd.


OM protein - protein search, using sw model

Run on:         March 13, 2003, 14:46:09 ; Search time 14.2463 Seconds
                                          (without alignments)
                                          171.421 Million cell updates/sec

Title:          US-09-636-530-2
Perfect score:  422
Sequence:       1 VSEIQLMHNLGKHLNSMERV..........KSLGEANKADVNVLTKAKSQ 83

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters:      262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Issued_Patents_AA:*
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                2:  /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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                4:  /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
                5:  /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                6:  /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

                              SUMMARIES
                %
Result          Query
   No.  Score   Match Length DB  ID                            Description
-------------------------------------------------------------------------------
     1    417    98.8     84  1  US-07-863-014-2                Sequence 2, Appli
     2    417    98.8     84  1  US-08-332-453-2                Sequence 2, Appli
     3    417    98.8     84  1  US-08-689-190-2                Sequence 2, Appli
     4    417    98.8     84  2  US-08-835-231-9                Sequence 9, Appli
     5    417    98.8     84  2  US-08-805-918-3                Sequence 3, Appli
     6    417    98.8     84  4  US-09-108-661-9                Sequence 9, Appli
     7    417    98.8     84  5  PCT-US95-15800-25              Sequence 25, Appl
     8    412    97.6     84  2  US-08-142-551B-1               Sequence 1, Appli
     9    412    97.6     84  2  US-08-411-726-1                Sequence 1, Appli
    10    407    96.4     84  1  US-07-707-114-1                Sequence 1, Appli
    11    368    87.2     84  1  US-07-773-098-2                Sequence 2, Appli
    12    364    86.3     84  2  US-08-733-446-5                Sequence 5, Appli
    13    359    85.1     84  1  US-07-773-098-1                Sequence 1, Appli
    14    356    84.4     81  2  US-08-733-446-4                Sequence 4, Appli
    15    352    83.4     84  1  US-07-776-272-14               Sequence 14, Appl
    16    351    83.2     80  2  US-08-733-446-3                Sequence 3, Appli
    17    350    82.9     84  1  US-07-773-098-9                Sequence 9, Appli
    18    350    82.9     84  1  US-07-773-098-10               Sequence 10, Appl
    19    347    82.2     79  2  US-08-733-446-2                Sequence 2, Appli
    20    342    81.0     78  2  US-08-733-446-1                Sequence 1, Appli
    21    341    80.8     84  1  US-07-773-098-7                Sequence 7, Appli
    22    341    80.8     84  1  US-07-773-098-8                Sequence 8, Appli
    23    337    79.9     84  3  US-09-044-536A-36              Sequence 36, Appl
    24    248    58.8     51  3  US-09-044-536A-7               Sequence 7; Appli
    25    237    56.2     50  2  US-08-142-551B-119             Sequence 119, App
    26    193    45.7     38  1  US-08-112-024-1                Sequence 1, Appli
    27    193    45.7     38  1  US-08-232-849-1                Sequence 1, Appli
    28    193    45.7     38  2  US-08-625-586-1                Sequence 1, Appli
    29    193    45.7     38  3  US-09-128-401-1                Sequence 1, Appli
    30    187    44.3     37  1  US-08-440-117-1                Sequence 1, Appli
    31    187    44.3     37  4  US-09-068-738A-16              Sequence 16, Appl
    32    186    44.1     38  5  PCT-US95-15800-29              Sequence 29, Appl
    33    183    43.4     36  1  US-08-256-363-4                Sequence 4, Appli
    34    179    42.4     34  1  US-08-256-363-2                Sequence 2, Appli
    35    179    42.4     35  1  US-08-256-363-3                Sequence 3, Appli
    36    179    42.4     36  1  US-08-112-024-2                Sequence 2, Appli
    37    175    41.5     33  1  US-08-256-363-1                Sequence 1, Appli
    38    175    41.5     34  1  US-07-765-373-1                Sequence 1, Appli
    39    175    41.5     34  1  US-08-033-099-1                Sequence 1, Appli
    40    175    41.5     34  1  US-08-262-495C-1               Sequence 1, Appli
    41    175    41.5     34  1  US-07-915-247A-1               Sequence 1, Appli
    42    175    41.5     34  1  US-08-443-863-1                Sequence 1, Appli
    43    175    41.5     34  1  US-08-448-070-1                Sequence 1, Appli
    44    175    41.5     34  1  US-08-488-105-7                Sequence 7, Appli
    45    175    41.5     34  1  US-08-468-275-6                Sequence 6, Appli


                              ALIGNMENTS


RESULT 1
US-07-863-014-2
; Sequence 2, Application US/07863014
; Patent No. 5382658
;  GENERAL INFORMATION:
;    APPLICANT:  KRONIS, K. Anne
;    APPLICANT:  BOZZATO, Richard P.
;    TITLE OF INVENTION:  STABILITY-ENHANCED VARIANTS OF
;    TITLE OF INVENTION:  PARATHYROID HORMONE
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  1800 Diagonal Road, Suite 500
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  USA
;      ZIP:  22313-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/863,014
;      FILING DATE:  19920403
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  16777/163 ALLE
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)836-9300
;      TELEFAX:  (703)683-4109
;      TELEX:  899149
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  84 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-07-863-014-2

  Query Match             98.8%;  Score 417;  DB 1;  Length 84;
  Best Local Similarity   98.8%;  Pred. No. 1.4e-44;
  Matches   82;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
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Db          2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 61
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Qy      61 SHEKSLGEANKADVNVLTKAKSQ 83
           |||||||||:|||||||||||||
Db      62 SHEKSLGEADKADVNVLTKAKSQ 84


RESULT 2
US-08-332-453-2
; Sequence 2, Application US/08332453
; Patent No. 5599792
;  GENERAL INFORMATION:
;    APPLICANT:  KRONIS, K. Anne
;    APPLICANT:  BOZZATO, Richard P.
;    TITLE OF INVENTION:  BONE-STIMULATING, NON-VASOACTIVE
;    TITLE OF INVENTION:  PARATHYROID HORMONE VARINATS
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  1800 Diagonal Road, Suite 500
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/332,453
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/900,680
;      FILING DATE:  19-JUN-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  16777/182 ALLE
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)836-9300
;      TELEFAX:  (703)683-4109
;      TELEX:  899149
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  84 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-332-453-2

  Query Match             98.8%;  Score 417;  DB 1;  Length 84;
  Best Local Similarity   98.8%;  Pred. No. 1.4e-44;
  Matches   82;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 61

Qy      61 SHEKSLGEANKADVNVLTKAKSQ 83
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Db      62 SHEKSLGEADKADVNVLTKAKSQ 84


RESULT 3
US-08-689-190-2
; Sequence 2, Application US/08689190
; Patent No. 5714349
;  GENERAL INFORMATION:
;    APPLICANT:  FUKUDA, Tsunehiko
;    APPLICANT:  OSHIKA, Yuri
;    APPLICANT:  YAMADA, Takao
;    TITLE OF INVENTION:  SYNTHETIC GENE CODING FOR HUMAN
;    TITLE OF INVENTION:  PARATHYROID HORMONE
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
;      ADDRESSEE:  CUSHMAN
;      STREET:  130 Water Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  US
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/689,190
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/006,197
;      FILING DATE:
;      APPLICATION NUMBER:  US/08/016,171
;      FILING DATE:
;      APPLICATION NUMBER:  US/07/765,371
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WILLIAMS, Gregory D
;      REGISTRATION NUMBER:  30,901
;      REFERENCE/DOCKET NUMBER:  41,288
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)523-3400
;      TELEFAX:  (617)523-6440
;      TELEX:  200291 STRE UR
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  84 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-689-190-2

  Query Match             98.8%;  Score 417;  DB 1;  Length 84;
  Best Local Similarity   98.8%;  Pred. No. 1.4e-44;
  Matches   82;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
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Db       2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 61

Qy      61 SHEKSLGEANKADVNVLTKAKSQ 83
           |||||||||:|||||||||||||
Db      62 SHEKSLGEADKADVNVLTKAKSQ 84


RESULT 4
US-08-835-231-9
; Sequence 9, Application US/08835231
; Patent No. 5861284
;  GENERAL INFORMATION:
;    APPLICANT:  NISHIMURA, Osamu
;    APPLICANT:  KURIYAMA, Masato
;    APPLICANT:  KOYAMA, No. 5861284uyuki
;    APPLICANT:  FUKUDA, Tsunehiko
;    TITLE OF INVENTION:  METHOD FOR PRODUCING A BIOLOGICALLY
;    TITLE OF INVENTION:  ACTIVE RECOMBINANT CYSTEINE-FREE
;    NUMBER OF SEQUENCES:  37
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
;      STREET:  130 WATER STREET
;      CITY:  BOSTON
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
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;       MEDIUM TYPE:  Diskette
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  DOS
;       SOFTWARE:  FastSEQ Version 1.5
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/835,231
;       FILING DATE:
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/350,709
;       FILING DATE:  07-DEC-1994
;       APPLICATION NUMBER:  07/838,857
;       FILING DATE:  18-FEB-1992
;       APPLICATION NUMBER:  JP 024841
;       FILING DATE:  19-FEB-1991
;       APPLICATION NUMBER:  JP 0271438
;       FILING DATE:  18-OCT-1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  DAVID, RESNICK S
;       REGISTRATION NUMBER:  34,235
;       REFERENCE/DOCKET NUMBER:  41614-FWC
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  617-523-3400
;       TELEFAX:  617-523-6440
;       TELEX:  200291 STRE
;   INFORMATION FOR SEQ ID NO:  9:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  84 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
;     FRAGMENT TYPE:  N-terminal
;     ORIGINAL SOURCE:
US-08-835-231-9

  Query Match             98.8%;  Score 417;  DB 2;  Length 84;
  Best Local Similarity   98.8%;  Pred. No. 1.4e-44;
  Matches   82;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 61

Qy       61 SHEKSLGEANKADVNVLTKAKSQ 83
            |||||||||:|||||||||||||
Db       62 SHEKSLGEADKADVNVLTKAKSQ 84

RESULT 5
US-08-805-918-3
; Sequence 3, Application US/08805918
; Patent No. 5885821
;  GENERAL INFORMATION:
;     APPLICANT:  MAGOTA, Koji
;     APPLICANT:  MASUDA, Toyofumi
;     APPLICANT:  SUZUKI, Yuji
;     APPLICANT:  YABUTA, Masayuki
;     TITLE OF INVENTION:  PROCESS FOR PRODUCTION OF SECRETORY KEX2
;     TITLE OF INVENTION:  DERIVATIVES
;     NUMBER OF SEQUENCES:  45
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  BURNS, DOANE, SWECKER & MATHIS
;       STREET:  P.O. Box 1404
;       CITY:  Alexandria
;       STATE:  Virginia
;       COUNTRY:  United States
;       ZIP:  22313-1404
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
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;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/805,918
;       FILING DATE:  04-MAR-1997
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 8-073217
;       FILING DATE:  04-MAR-1996
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 8-352580
;       FILING DATE:  16-DEC-1996
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Meuth, Donna M.
;       REGISTRATION NUMBER:  36,607
;       REFERENCE/DOCKET NUMBER:  001560-295
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (703) 836-6620
;       TELEFAX:  (703) 836-2021
;   INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  84 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-08-805-918-3

  Query Match             98.8%;  Score 417;  DB 2;  Length 84;
  Best Local Similarity   98.8%;  Pred. No. 1.4e-44;
  Matches   82;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
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Db        2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 61

Qy       61 SHEKSLGEANKADVNVLTKAKSQ 83
            |||||||||:|||||||||||||
Db       62 SHEKSLGEADKADVNVLTKAKSQ 84

RESULT 6
US-09-108-661-9
; Sequence 9, Application US/09108661
; Patent No. 6287806
;  GENERAL INFORMATION:
;     APPLICANT:  NISHIMURA, Osamu
;     APPLICANT:  KURIYAMA, Masato
;     APPLICANT:  KOYAMA, No. 6287806uyuki
;     APPLICANT:  FUKUDA, Tsunehiko
;     TITLE OF INVENTION:  METHOD FOR PRODUCING A BIOLOGICALLY
;     TITLE OF INVENTION:  ACTIVE RECOMBINANT CYSTEINE-FREE
;     NUMBER OF SEQUENCES:  37
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
;       STREET:  130 WATER STREET
;       CITY:  BOSTON
;       STATE:  MA
;       COUNTRY:  USA
;       ZIP:  02109
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  DOS
;       SOFTWARE:  FastSEQ Version 1.5
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/108,661
;       FILING DATE:
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/350,709
;       FILING DATE:  07-DEC-1994
;       APPLICATION NUMBER:  07/838,857
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;       FILING DATE:  18-FEB-1992
;       APPLICATION NUMBER:  JP 024841
;       FILING DATE:  19-FEB-1991
;       APPLICATION NUMBER:  JP 0271438
;       FILING DATE:  18-OCT-1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  DAVID, RESNICK S
;       REGISTRATION NUMBER:  34,235
;       REFERENCE/DOCKET NUMBER:  41614-FWC
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  617-523-3400
;       TELEFAX:  617-523-6440
;       TELEX:  200291 STRE
;   INFORMATION FOR SEQ ID NO:  9:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  84 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
;     FRAGMENT TYPE:  N-terminal
;     ORIGINAL SOURCE:
US-09-108-661-9

  Query Match             98.8%;  Score 417;  DB 4;  Length 84;
  Best Local Similarity   98.8%;  Pred. No. 1.4e-44;
  Matches   82;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
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Db       2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 61

Qy      61 SHEKSLGEANKADVNVLTKAKSQ 83
           |||||||||:|||||||||||||
Db      62 SHEKSLGEADKADVNVLTKAKSQ 84


RESULT 7
PCT-US95-15800-25
; Sequence 25, Application PC/TUS9515800
;  GENERAL INFORMATION:
;     APPLICANT:  BioNebraska, Inc.
;     TITLE OF INVENTION:  PRODUCTION OF PEPTIDES USING
;     TITLE OF INVENTION:  RECOMBINANT FUSION PROTEIN CONSTRICTS
;     NUMBER OF SEQUENCES:  33
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Merchant & Gould
;       STREET:  3100 Norwest Center, 90 S. 7th Street
;       CITY:  Minneapolis
;       STATE:  MN
;       COUNTRY:  U.S.A.
;       ZIP:  55402
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  DOS
;       SOFTWARE:  FastSEQ Version 1.5
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US95/15800
;       FILING DATE:  07-DEC-1995
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/350,530
;       FILING DATE:  07-DEC-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Carter, Charles G
;       REGISTRATION NUMBER:  35,093
;       REFERENCE/DOCKET NUMBER:  8648.45USWO
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  612/332-5300
;       TELEFAX:  612/332-9081
```

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;       TELEX:
;   INFORMATION FOR SEQ ID NO:  25:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  84 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
;     FRAGMENT TYPE:  internal
;     ORIGINAL SOURCE:
PCT-US95-15800-25

  Query Match             98.8%;  Score 417;  DB 5;  Length 84;
  Best Local Similarity   98.8%;  Pred. No. 1.4e-44;
  Matches   82;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 61

Qy      61 SHEKSLGEANKADVNVLTKAKSQ 83
           |||||||||:|||||||||||||
Db      62 SHEKSLGEADKADVNVLTKAKSQ 84


RESULT 8
US-08-142-551B-1
; Sequence 1, Application US/08142551B
; Patent No. 5814603
;  GENERAL INFORMATION:
;     APPLICANT:  Oldenburg, Kevin R.
;     APPLICANT:  Selick, Harold E.
;     TITLE OF INVENTION:  COMPOUNDS WITH PTH ACTIVITY AND
;     TITLE OF INVENTION:  RECOMBINANT DNA VECTORS ENCODING SAME
;     NUMBER OF SEQUENCES:  132
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Burns, Doane, Swecker & Mathis
;       STREET:  699 Prince Street
;       CITY:  Alexandria
;       STATE:  Virginia
;       COUNTRY:  US
;       ZIP:  22313
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/142,551B
;       FILING DATE:  25-OCT-1993
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/077,296
;       FILING DATE:  14-JUN-1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/898,219
;       FILING DATE:  12-JUN-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/965,677
;       FILING DATE:  22-OCT-1992
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Swiss, Gerald F.
;       REGISTRATION NUMBER:  30,113
;       REFERENCE/DOCKET NUMBER:  000324-010
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (415) 854-7400
;       TELEFAX:  (415) 854-8275
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  84 amino acids
;       TYPE:  amino acid
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;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  Protein
;      LOCATION:  1..84
;      OTHER INFORMATION:  /note= "84 amino acid PTH"
US-08-142-551B-1

  Query Match             97.6%;  Score 412;  DB 2;  Length 84;
  Best Local Similarity   97.6%;  Pred. No. 5.9e-44;
  Matches   81;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 61

Qy       61 SHEKSLGEANKADVNVLTKAKSQ 83
            |||||||||:||||:||||||||
Db       62 SHEKSLGEADKADVDVLTKAKSQ 84


RESULT 9
US-08-411-726-1
; Sequence 1, Application US/08411726
; Patent No. 5880093
;  GENERAL INFORMATION:
;    APPLICANT:  BAGNOLI, Franco
;    TITLE OF INVENTION:  Use of Parathormone, Its Biologically
;    TITLE OF INVENTION:  Active Fragments and Correlated Peptides, for The Preparation
;    TITLE OF INVENTION:  Pharmaceutical Compositions Useful for The Treatment of Pregna
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Kenyon & Kenyon
;      STREET:  1 Broadway
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  US
;      ZIP:  10004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS 6.2
;      SOFTWARE:  WordPerfect 6.1 for Windows
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/411,726
;      FILING DATE:  05-APR-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP93/02755
;      FILING DATE:  08-OCT-1993
;      APPLICATION NUMBER:  MI-92A002331
;      FILING DATE:  09-OCT-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  PALMESE, Maria Luisa
;      REGISTRATION NUMBER:  34,402
;      REFERENCE/DOCKET NUMBER:  2111/1300
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-425-7200
;      TELEFAX:  212-425-5288
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  84 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-411-726-1

  Query Match             97.6%;  Score 412;  DB 2;  Length 84;
  Best Local Similarity   97.6%;  Pred. No. 5.9e-44;
  Matches   81;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 61

Qy       61 SHEKSLGEANKADVNVLTKAKSQ 83
            |||||||||:||||:||||||||
Db       62 SHEKSLGEADKADVDVLTKAKSQ 84

RESULT 10
US-07-707-114-1
; Sequence 1, Application US/07707114
; Patent No. 5208041
;  GENERAL INFORMATION:
;    APPLICANT:  SINDREY, Dennis R.
;    TITLE OF INVENTION:  ESSENTIALLY PURE HUMAN PARATHYROID
;    TITLE OF INVENTION:  HORMONE
;    NUMBER OF SEQUENCES:  1
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  1800 Diagonal Road, Suite 500
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/707,114
;      FILING DATE:  19910523
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  16777/147 ALLE
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)836-9300
;      TELEFAX:  (703)683-4109
;      TELEX:  899149
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  84 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    ORIGINAL SOURCE:
;      ORGANISM:  homo sapiens
;    IMMEDIATE SOURCE:
;      CLONE:  hPTH
US-07-707-114-1

  Query Match             96.4%;  Score 407;  DB 1;  Length 84;
  Best Local Similarity   96.4%;  Pred. No. 2.5e-43;
  Matches   80;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 61

Qy       61 SHEKSLGEANKADVNVLTKAKSQ 83
            |||||||||:||:|:||||||||
Db       62 SHEKSLGEADKANVDVLTKAKSQ 84

RESULT 11
US-07-773-098-2
; Sequence 2, Application US/07773098
; Patent No. 5317010
;  GENERAL INFORMATION:
;    APPLICANT:  PANG, Peter K.T.
;    APPLICANT:  JIE, Shan
```

```
;    TITLE OF INVENTION:  PARATHYROID HORMONE ANALOGUES AS
;    TITLE OF INVENTION:  OSTEOPOROTIC CONTROL AGENTS
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Armstrong, Nikaido, Marmelstein, Kubovcik &
;      ADDRESSEE:  Murray
;      STREET:  1725 K Street, N.W., Suite 1000
;      CITY:  Washington D.C.
;      COUNTRY:  United States of America
;      ZIP:  20006
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/773,098
;      FILING DATE:  19911010
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murray, Robert B.
;      REGISTRATION NUMBER:  22,890
;      REFERENCE/DOCKET NUMBER:  901930
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 659-2930
;      TELEFAX:  (202) 887-0357
;      TELEX:  440142
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  84 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-07-773-098-2

  Query Match             87.2%;  Score 368;  DB 1;  Length 84;
  Best Local Similarity   88.0%;  Pred. No. 1.7e-38;
  Matches   73;  Conservative    4;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
             |||||||||||||||||||||||||||||||||||||| :| ||  ||||||||||||||
Db       2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGASIAYRDGSSQRPRKKEDNVLVE 61

Qy      61 SHEKSLGEANKADVNVLTKAKSQ 83
             ||:||||||:||||:|| ||| |
Db      62 SHQKSLGEADKADVDVLIKAKPQ 84


RESULT 12
US-08-733-446-5
; Sequence 5, Application US/08733446
; Patent No. 5856138
;  GENERAL INFORMATION:
;    APPLICANT:  FUKUDA, Tsunehiko
;    TITLE OF INVENTION:  HUMAN PARATHYROID HORMONE MUTEINS AND
;    TITLE OF INVENTION:  PRODUCTION THEREOF
;    NUMBER OF SEQUENCES:  62
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
;      ADDRESSEE:  CUSHMAN
;      STREET:  130 Water Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  US
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/733,446
;      FILING DATE:  18-OCT-1996
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;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/402,970
;      FILING DATE:
;      APPLICATION NUMBER:  US/07/926,787
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  NEUNER, George W
;      REGISTRATION NUMBER:  26964
;      REFERENCE/DOCKET NUMBER:  42025
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)523-3400
;      TELEFAX:  (617)523-6440
;      TELEX:  200291 STRE UR
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  84 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  mutation
;      LOCATION:  8 Xaa=Leu, Ile, Val, Phe, Tyr, Trp or Met,
;      LOCATION:  18 Xaa=Leu, Ile, Val, Phe, Tyr, Trp or Met,
;      LOCATION:  34 Xaa=Cys or Phe,  35 Xaa=Cys or Val,
;      LOCATION:  37 Xaa=Cys or Leu,  39 Xaa=Cys or Ala,
;      LOCATION:  41 Xaa=Cys or Leu,  43 Xaa=Cys or Pro, 44 Xaa=Cys or Arg
;      IDENTIFICATION METHOD:  E
US-08-733-446-5

  Query Match             86.3%;  Score 364;  DB 2;  Length 84;
  Best Local Similarity   88.0%;  Pred. No. 5.3e-38;
  Matches   73;  Conservative    1;  Mismatches    9;  Indels    0;  Gaps    0;

Qy       1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
             |||||| ||||||||| |||||||||||||||  | | | |  |||||||||||||||||
Db       2 VSEIQLXHNLGKHLNSXERVEWLRKKLQDVHNXXAXGXPXAXXDAGSQRPRKKEDNVLVE 61

Qy      61 SHEKSLGEANKADVNVLTKAKSQ 83
             |||||||||:|||||||||||||
Db      62 SHEKSLGEADKADVNVLTKAKSQ 84


RESULT 13
US-07-773-098-1
; Sequence 1, Application US/07773098
; Patent No. 5317010
;  GENERAL INFORMATION:
;    APPLICANT:  PANG, Peter K.T.
;    APPLICANT:  JIE, Shan
;    TITLE OF INVENTION:  PARATHYROID HORMONE ANALOGUES AS
;    TITLE OF INVENTION:  OSTEOPOROTIC CONTROL AGENTS
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Armstrong, Nikaido, Marmelstein, Kubovcik &
;      ADDRESSEE:  Murray
;      STREET:  1725 K Street, N.W., Suite 1000
;      CITY:  Washington D.C.
;      COUNTRY:  United States of America
;      ZIP:  20006
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/773,098
;      FILING DATE:  19911010
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murray, Robert B.
;      REGISTRATION NUMBER:  22,890
;      REFERENCE/DOCKET NUMBER:  901930
```

```
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 659-2930
;      TELEFAX:  (202) 887-0357
;      TELEX:  440142
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  84 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-07-773-098-1

  Query Match             85.1%;  Score 359;  DB 1;  Length 84;
  Best Local Similarity   85.5%;  Pred. No. 2.2e-37;
  Matches   71;  Conservative    5;  Mismatches    7;  Indels    0;  Gaps    0;

Qy      1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
          ||||| ||||||||:||||||||||||||||||||||| :| ||  ||||||||||||||
Db      2 VSEIQFMHNLGKHLSSMERVEWLRKKLQDVHNFVALGASIAYRDGSSQRPRKKEDNVLVE 61

Qy     61 SHEKSLGEANKADVNVLTKAKSQ 83
          ||:||||||:||||:|| ||| |
Db     62 SHQKSLGEADKADVDVLIKAKPQ 84


RESULT 14
US-08-733-446-4
; Sequence 4, Application US/08733446
; Patent No. 5856138
;  GENERAL INFORMATION:
;    APPLICANT:  FUKUDA, Tsunehiko
;    TITLE OF INVENTION:  HUMAN PARATHYROID HORMONE MUTEINS AND
;    TITLE OF INVENTION:  PRODUCTION THEREOF
;    NUMBER OF SEQUENCES:  62
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
;      ADDRESSEE:  CUSHMAN
;      STREET:  130 Water Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  US
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/733,446
;      FILING DATE:  18-OCT-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/402,970
;      FILING DATE:
;      APPLICATION NUMBER:  US/07/926,787
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  NEUNER, George W
;      REGISTRATION NUMBER:  26964
;      REFERENCE/DOCKET NUMBER:  42025
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)523-3400
;      TELEFAX:  (617)523-6440
;      TELEX:  200291 STRE UR
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  81 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  mutation
;      LOCATION:  5 Xaa=Leu, Ile, Val, Phe, Tyr, Trp or Met,
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;      LOCATION:  15 Xaa=Leu, Ile, Val, Phe, Tyr, Trp or Met,
;      LOCATION:  31 Xaa=Cys or Phe,  32 Xaa=Cys or Val,
;      LOCATION:  34 Xaa=Cys or Leu,  36 Xaa=Cys or Ala,
;      LOCATION:  38 Xaa=Cys or Leu,  40 Xaa=Cys or Pro, 41 Xaa=Cys or Arg
;      IDENTIFICATION METHOD:  E
US-08-733-446-4

  Query Match             84.4%;  Score 356;  DB 2;  Length 81;
  Best Local Similarity   87.7%;  Pred. No. 5e-37;
  Matches   71;  Conservative    1;  Mismatches    9;  Indels    0;  Gaps    0;

Qy      3 EIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVESH 62
          |||| ||||||||| |||||||||||||||  | | | |  |||||||||||||||||||
Db      1 EIQLXHNLGKHLNSXERVEWLRKKLQDVHNXXAXGXPXAXXDAGSQRPRKKEDNVLVESH 60

Qy     63 EKSLGEANKADVNVLTKAKSQ 83
          |||||||:|||||||||||||
Db     61 EKSLGEADKADVNVLTKAKSQ 81


RESULT 15
US-07-776-272-14
; Sequence 14, Application US/07776272
; Patent No. 5612454
;  GENERAL INFORMATION:
;    APPLICANT:  Kaminuma, Toshihiko
;    APPLICANT:  Iida, Toshii
;    APPLICANT:  Tajima, Masahiro
;    TITLE OF INVENTION:  Process for Purification of Polypeptide
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wegner, Cantor, Mueller & Player
;      STREET:  1233 20th St. N.W.  P.O. Box 18218
;      CITY:  Washington
;      STATE:  District of Columbia
;      COUNTRY:  United States of America
;      ZIP:  20036-8218
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/776,272
;      FILING DATE:  19911129
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Player, William E
;      REGISTRATION NUMBER:  31,409
;      REFERENCE/DOCKET NUMBER:  P-450-23167
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-887-0400
;      TELEFAX:  202-887-0605
;      TELEX:  440706
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  84 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  YES
;    ORIGINAL SOURCE:
;      ORGANISM:  Swine
US-07-776-272-14

  Query Match             83.4%;  Score 352;  DB 1;  Length 84;
  Best Local Similarity   83.1%;  Pred. No. 1.6e-36;
  Matches   69;  Conservative    7;  Mismatches    7;  Indels    0;  Gaps    0;

Qy      1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
          ||||||||||||||:|:|||:||||||||||||||||| :  || |||||||||||||||
Db      2 VSEIQLMHNLGKHLSSLERVQWLRKKLQDVHNFVALGASIVHRDGGSQRPRKKEDNVLVE 61
```

```
Qy     61 SHEKSLGEANKADVNVLTKAKSQ 83
          ||:||||||:|| |:|| ||| |
Db     62 SHQKSLGEADKAAVDVLIKAKPQ 84

Search completed: March 13, 2003, 14:52:54
Job time : 15.2463 secs
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                    GenCore version 5.1.4_p5_4578
             Copyright (c) 1993 - 2003  Compugen Ltd.


OM protein - protein search, using sw model

Run on:         March 13, 2003, 14:58:49 ; Search time 16.1045 Seconds
                                           (without alignments)
                                           495.462 Million cell updates/sec

Title:          US-09-636-530-2
Perfect score:  422
Sequence:       1 VSEIQLMHNLGKHLNSMERV..........KSLGEANKADVNVLTKAKSQ 83

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters:      283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       PIR_73:*
                1:  pir1:*
                2:  pir2:*
                3:  pir3:*
                4:  pir4:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                SUMMARIES
                   %
Result           Query
  No.   Score   Match Length DB  ID                  Description
-----------------------------------------------------------------------------
    1     417    98.8    115  1  PTHU                parathyroid hormon
    2     366    86.7    115  2  JC4202              parathyroid hormon
    3     359    85.1    115  1  PTBO                parathyroid hormon
    4     355    84.1    115  1  PTPG                parathyroid hormon
    5     311    73.7    115  2  A05091              parathyroid hormon
    6     303    71.8    105  2  I51851              parathyroid hormon
    7   174.5    41.4    119  2  A34937              parathyroid hormon
    8      73    17.3    565  2  G89813              DNA polymerase III
    9    72.5    17.2    824  2  F72408              leucine-tRNA ligas
   10      72    17.1   1257  1  I58383              retinoblastoma bin
   11    69.5    16.5    555  2  T44010              virion protein [im
   12    67.5    16.0   1156  2  B70356              chromosome assembl
   13      67    15.9    443  2  E82046              proteinase HslVU,
   14      67    15.9    655  2  C71438              hypothetical prote
   15      67    15.9    674  2  B71438              hypothetical prote
   16    66.5    15.8    378  2  F56653              virion protein - h
   17      66    15.6    215  2  T23195              hypothetical prote
   18      66    15.6    396  2  G96934              DNA-damage repair
   19      66    15.6   1163  2  F84669              probable chromosom
   20      65    15.4    283  2  H86803              prophage pi3 prote
   21      65    15.4   1244  2  T23744              chromosome-associa
   22    64.5    15.3    205  2  A86506              GMP kinase [import
   23    64.5    15.3    205  2  F72117              guanylate kinase C
   24    64.5    15.3   1018  2  T40253              hypothetical prote
   25      64    15.2    166  2  T43497              hypothetical prote
   26      64    15.2    642  2  D81401              probable flagellar
   27    63.5    15.0    417  2  E70207              antigen S1 - Lyme
   28    63.5    15.0    487  2  A71407              probable Ste20-lik
   29    63.5    15.0    797  2  A96232              succinoglycan bios
   30    63.5    15.0    797  2  AD3054              hypothetical prote
   31    63.5    15.0   1270  2  T09194              adaptor protein in
   32      63    14.9    108  2  T37558              probable methyltra
   33      63    14.9    672  2  T42186              conserved hypothet
   34      63    14.9    862  2  A05028              rpoC protein homol
   35      63    14.9    992  2  A39931              protein-tyrosine k
   36      63    14.9   1000  2  S18827              Flt3 protein - mou
   37      63    14.9   1033  2  S73693              MG328 homolog P01_
   38      63    14.9   1937  2  I38055              myosin heavy chain
   39      63    14.9   2109  2  I38414              transcription fact
   40      63    14.9   5005  2  F82884              hypothetical prote
   41    62.5    14.8    370  1  D64650              probable membrane-
   42    62.5    14.8    415  2  T34156              hypothetical prote
   43    62.5    14.8    509  2  T29291              hypothetical prote
   44    62.5    14.8    673  2  S54182              low affinity penic
   45    62.5    14.8    674  2  S54178              low affinity penic


                                ALIGNMENTS


RESULT 1
PTHU
parathyroid hormone precursor [validated] - human
N;Alternate names: proparathyroid hormone
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 19-Jan-1996 #text_change 08-Dec-2000
C;Accession: A19339; S53790; A93169; S21199; A93789; A93783; A90387; A90426; A94410;
R;Vasicek, T.J.; McDevitt, B.E.; Freeman, M.W.; Fennick, B.J.; Hendy, G.N.; Potts Jr.
Proc. Natl. Acad. Sci. U.S.A. 80, 2127-2131, 1983
A;Title: Nucleotide sequence of the human parathyroid hormone gene.
A;Reference number: A19339; MUID:83169834; PMID:6220408
A;Accession: A19339
A;Molecule type: DNA
A;Residues: 1-115 <VAS>
A;Cross-references: GB:J00301; NID:g190702; PIDN:AAA60215.1; PID:g190704
R;Yamaguchi, T.; Fukase, M.; Sugimoto, T.; Kido, H.; Chihara, K.
Biol. Chem. Hoppe-Seyler 375, 821-824, 1994
A;Title: Purification of meprin from human kidney and its role in parathyroid hormone
A;Reference number: S53790; MUID:95225988; PMID:7710697
A;Accession: S53790
A;Molecule type: protein
A;Residues: 'X',33,'X',35-46;65-84;105-110 <YAM>
A;Note: peptides generated in vitro and in vivo by meprin; peptide cleavage also occu
R;Jacobs, J.W.; Kemper, B.; Niall, H.D.; Habener, J.F.; Potts Jr., J.T.
Nature 249, 155-157, 1974
A;Title: Structural analysis of human proparathyroid hormone by a new microsequencing
A;Reference number: A93169; MUID:74174967; PMID:4833516
A;Accession: A93169
A;Molecule type: protein
A;Residues: 26-37 <JAC>
R;Olstad, O.K.; Reppe, S.; Gabrielsen, O.S.; Hartmanis, M.; Blingsmo, O.R.; Gautvik,
Eur. J. Biochem. 205, 311-319, 1992
A;Title: Isolation and characterization of two biologically active O-glycosylated for
ation.
A;Reference number: S21199; MUID:92209518; PMID:1555591
A;Accession: S21199
A;Molecule type: protein
A;Residues: 32-114,'N' <OLS>
A;Note: cloned sequence expressed in Saccharomyces cerevisiae exhibited O-glycosylati
R;Niall, H.D.; Sauer, R.T.; Jacobs, J.W.; Keutmann, H.T.; Segre, G.V.; O'Riordan, J.L
Proc. Natl. Acad. Sci. U.S.A. 71, 384-388, 1974
A;Title: The amino-acid sequence of the amino-terminal 37 residues of human parathyro
A;Reference number: A93789; MUID:74111656; PMID:4521809
A;Accession: A93789
A;Molecule type: protein
A;Residues: 32-68 <NIA>
R;Brewer Jr., H.B.; Fairwell, T.; Ronan, R.; Sizemore, G.W.; Arnaud, C.D.
Proc. Natl. Acad. Sci. U.S.A. 69, 3585-3588, 1972
A;Title: Human parathyroid hormone: amino-acid sequence of the amino-terminal residue
A;Reference number: A93783; MUID:73070429; PMID:4509319
A;Accession: A93783
A;Molecule type: protein
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A;Residues: 32-52,'Q',54-58,'K',60,'L',62-65 <BRE>
A;Note: this sequence was determined by sequenator and mass spectroscopic identificatio
R;Keutmann, H.T.; Niall, H.D.; O'Riordan, J.L.H.; Potts Jr., J.T.
Biochemistry 14, 1842-1847, 1975
A;Title: A reinvestigation of the amino-terminal sequence of human parathyroid hormone.
A;Reference number: A90387; MUID:75146516; PMID:1125201
A;Accession: A90387
A;Molecule type: protein
A;Residues: 52-75 <KE3>
R;Keutmann, H.T.; Sauer, M.M.; Hendy, G.N.; O'Riordan, J.L.H.; Potts Jr., J.T.
Biochemistry 17, 5723-5729, 1978
A;Title: Complete amino acid sequence of human parathyroid hormone.
A;Reference number: A90426; MUID:79082855; PMID:728431
A;Accession: A90426
A;Molecule type: protein
A;Residues: 61-106,'D',108-115 <KEU>
R;Keutmann, H.T.; Niall, H.D.; Jacobs, J.W.; Barling, P.M.; Hendy, G.N.; O'Riordan, J.L.
in Calcium-regulating Hormones, Talmadge, R.V., Owen, M., and Parsons, J.A., eds., pp.9
A;Reference number: A94410
A;Accession: A94410
A;Molecule type: protein
A;Residues: 75-100 <KE2>
R;Tregear, G.W.; van Rietschoten, J.; Green, E.; Niall, H.D.; Keutmann, H.T.; Parsons, J
Hoppe-Seyler's Z. Physiol. Chem. 355, 415-421, 1974
A;Title: Solid-phase synthesis of the biologically active N-terminal 1-34 peptide of hum
A;Reference number: A91660; MUID:75059220; PMID:4474131
A;Contents: annotation; synthesis of residues 32-65
A;Note: the biologically active amino-terminal 34 residues of parathyroid hormone were s
at renal adenylate cyclase assay and with the bovine hormone's active region in the chic
R;Andreatta, R.H.; Hartmann, A.; Joehl, A.; Kamber, B.; Maier, R.; Riniker, B.; Rittel,
Helv. Chim. Acta 56, 470-473, 1973
A;Title: Synthese der Sequenz 1-34 von menschlichem Parat-hormon.
A;Reference number: A91635; MUID:73227467; PMID:4721748
A;Contents: annotation; synthesis of residues 32-65
A;Note: the amino-terminal 34 residues of the parathyroid hormone sequence as determined
 into thyroparathyroidectomized rats caused a distinct increase in plasma calcium level
R;Hendy, G.N.; Kronenberg, H.M.; Potts, J.T.
Proc. Natl. Acad. Sci. U.S.A. 78, 7365-7369, 1981
A;Title: Nucleotide sequence of cloned cDNAs encoding human preproparathyroid hormone.
A;Reference number: I38342; MUID:82150870; PMID:6950381
A;Accession: I38342
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-115 <RES>
A;Cross-references: EMBL:V00597; NID:g37143; PIDN:CAA23843.1; PID:g37144
C;Genetics:
A;Gene: GDB:PTH
A;Cross-references: GDB:119522; OMIM:168450
A;Map position: 11p15.2-11p15.1
A;Introns: 29/2
A;Note: the first intron occurs before the initiator codon
C;Function:
A;Description: factor in homeostatic control of plasma calcium and phosphate; released b
 counter to calcitonin
C;Superfamily: parathyroid hormone; parathyroid hormone homology
C;Keywords: calcium; hormone; parathyroid gland; plasma
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-31/Domain: propeptide #status experimental <PRO>
F;30-64/Domain: parathyroid hormone homology <PTH>
F;32-115/Product: parathyroid hormone #status experimental <MAT>

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Qy      1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
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Db     33 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 92

Qy     61 SHEKSLGEANKADVNVLTKAKSQ 83
          |||||||||:|||||||||||||
Db     93 SHEKSLGEADKADVNVLTKAKSQ 115


RESULT 2
JC4202
parathyroid hormone precursor - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 10-Sep-1995 #sequence_revision 27-Oct-1995 #text_change 16-Jul-1999
C;Accession: JC4202
R;Rosol, T.J.; Steinmeyer, C.L.; McCauley, L.K.; Groene, A.; DeWille, J.W.; Capen, C.
Gene 160, 241-243, 1995
A;Title: Sequences of the cDNAs encoding canine parathyroid hormone-related protein a
A;Reference number: JC4201; MUID:95369696; PMID:7642102
A;Accession: JC4202
A;Molecule type: mRNA
A;Residues: 1-115 <ROS>
A;Cross-references: GB:U15662; NID:g558915; PIDN:AAA82584.1; PID:g558916
C;Superfamily: parathyroid hormone; parathyroid hormone homology
C;Keywords: hormone
F;1-31/Domain: signal sequence #status predicted <SIG>
F;30-64/Domain: parathyroid hormone homology <PTH>
F;32-115/Product: parathyroid hormone #status predicted <MAT>

  Query Match             86.7%;  Score 366;  DB 2;  Length 115;
  Best Local Similarity   86.7%;  Pred. No. 1.3e-31;
  Matches   72;  Conservative    6;  Mismatches    5;  Indels    0;  Gaps    0;

Qy      1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
          ||||| ||||||||:||||||||||||||||||||||||:| ||  |||| |||||||||
Db     33 VSEIQFMHNLGKHLSSMERVEWLRKKLQDVHNFVALGAPIAHRDGSSQRPLKKEDNVLVE 92

Qy     61 SHEKSLGEANKADVNVLTKAKSQ 83
          |::||||||:||||:||||||||
Db     93 SYQKSLGEADKADVDVLTKAKSQ 115


RESULT 3
PTBO
parathyroid hormone precursor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 18-Jun-1999
C;Accession: A24949; A93835; A93793; A91648; A93773; I45975; I45976; A01534
R;Weaver, C.A.; Gordon, D.F.; Kissil, M.S.; Mead, D.A.; Kemper, B.
Gene 28, 319-329, 1984
A;Title: Isolation and complete nucleotide sequence of the gene for bovine parathyroi
A;Reference number: A24949; MUID:84262483; PMID:6086460
A;Accession: A24949
A;Molecule type: DNA
A;Residues: 1-115 <WEA>
A;Cross-references: GB:K01938
R;Kronenberg, H.M.; McDevitt, B.E.; Majzoub, J.A.; Nathans, J.; Sharp, P.A.; Potts Jr
Proc. Natl. Acad. Sci. U.S.A. 76, 4981-4985, 1979
A;Title: Cloning and nucleotide sequence of DNA coding for bovine preproparathyroid h
A;Reference number: A93835; MUID:80056617; PMID:388425
A;Accession: A93835
A;Molecule type: DNA
A;Residues: 1-115 <KRO>
A;Cross-references: GB:V00106; GB:J00023; NID:g84; PIDN:CAA23439.1; PID:g85
A;Note: the authors translated the codon GAA for residue 50 as Gly
R;Hamilton, J.W.; Niall, H.D.; Jacobs, J.W.; Keutmann, H.T.; Potts Jr., J.T.; Cohn, D
Proc. Natl. Acad. Sci. U.S.A. 71, 653-656, 1974
A;Title: The N-terminal amino-acid sequence of bovine proparathyroid hormone.
A;Reference number: A93793; MUID:74142666; PMID:4522780
A;Accession: A93793
A;Molecule type: protein
A;Residues: 26-115 <HAM>
R;Niall, H.D.; Keutmann, H.T.; Sauer, R.; Hogan, M.L.; Dawson, B.F.; Aurbach, G.D.; P
Hoppe-Seyler's Z. Physiol. Chem. 351, 1586-1588, 1970
A;Title: The amino acid sequence of bovine parathyroid hormone I.
A;Reference number: A91648; MUID:71076162; PMID:5531031
A;Accession: A91648
A;Molecule type: protein
A;Residues: 32-115 <NIA>
R;Brewer Jr., H.B.; Ronan, R.
Proc. Natl. Acad. Sci. U.S.A. 67, 1862-1869, 1970
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A;Title: Bovine parathyroid hormone: amino acid sequence.
A;Reference number: A93773; MUID:71063634; PMID:5275384
A;Accession: A93773
A;Molecule type: protein
A;Residues: 32-115 <BRE>
R;Potts Jr., J.T.; Tregear, G.W.; Keutmann, H.T.; Niall, H.D.; Sauer, R.; Deftos, L.J.;
Proc. Natl. Acad. Sci. U.S.A. 68, 63-67, 1971
A;Title: Synthesis of a biologically active N-terminal tetratriacontapeptide of parathyr
A;Reference number: A93776; MUID:71091588; PMID:4322265
A;Contents: annotation; synthesis of residues 32-65
A;Note: the synthetic peptide was active in vivo and in vitro
R;Brewer Jr., H.B.; Fairwell, T.; Rittel, W.; Littledike, T.; Arnaud, C.D.
Am. J. Med. 56, 759-766, 1974
A;Title: Recent studies on the chemistry of human, bovine and porcine parathyroid hormon
A;Reference number: A90030; MUID:74173303; PMID:4598526
A;Contents: annotation
R;Weaver, C.A.; Gordon, D.F.
Proc. Natl. Acad. Sci. U.S.A. 78, 4073-4077, 1981
A;Title: introduction by molecular cloning of artifactual inverted sequences at the 5' t
A;Reference number: I45975; MUID:82037785; PMID:6170060
A;Accession: I45975
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-115 <WE2>
A;Cross-references: GB:J00024; NID:g163642; PIDN:AAA30747.1; PID:g163643
R;Weaver, C.A.; Gordon, D.F.
Mol. Cell. Endocrinol. 28, 411-424, 1982
A;Title: Nucleotide sequence of bovine parathyroid hormone messenger RNA.
A;Reference number: I45976; MUID:83105964; PMID:6185374
A;Accession: I45976
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-115 <WE3>
A;Cross-references: GB:M25082; NID:g163644; PIDN:AAA30748.1; PID:g163645
C;Genetics:
A;Gene: PTH
A;Introns: 29/2
C;Superfamily: parathyroid hormone; parathyroid hormone homology
C;Keywords: hormone
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-115/Product: proparathyroid hormone #status experimental <PMAT>
F;26-31/Domain: propeptide #status experimental <PRO>
F;30-64/Domain: parathyroid hormone homology <PTH>
F;32-115/Product: parathyroid hormone #status experimental <MAT>

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Db     33 VSEIQFMHNLGKHLSSMERVEWLRKKLQDVHNFVALGASIAYRDGSSQRPRKKEDNVLVE 92

Qy     61 SHEKSLGEANKADVNVLTKAKSQ 83
          ||:||||||:||||:|| ||| |
Db     93 SHQKSLGEADKADVDVLIKAKPQ 115


RESULT 4
PTPG
parathyroid hormone precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 24-Apr-1984 #sequence_revision 12-Apr-1996 #text_change 18-Jun-1999
C;Accession: B26806; A90390; A90376; A01535
R;Schmelzer, H.J.; Gross, G.; Widera, G.; Mayer, H.
Nucleic Acids Res. 15, 6740, 1987
A;Title: Nucleotide sequence of a full-length cDNA clone encoding preproparathyroid horm
A;Reference number: A26806; MUID:87316938; PMID:3628009
A;Accession: B26806
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-115 <SCH>
A;Cross-references: GB:X05722; GB:Y00409; NID:g1838; PIDN:CAA29193.1; PID:g1839
R;Chu, L.L.H.; Huang, W.Y.; Littledike, E.T.; Hamilton, J.W.; Cohn, D.V.
Biochemistry 14, 3631-3635, 1975
A;Title: Porcine proparathyroid hormone. Identification, biosynthesis, and partial am
A;Reference number: A90390; MUID:76018954; PMID:1164500
A;Accession: A90390
A;Molecule type: protein
A;Residues: 26-115 <CHU>
R;Sauer, R.T.; Niall, H.D.; Hogan, M.L.; Keutmann, H.T.; O'Riordan, J.L.H.; Potts Jr.
Biochemistry 13, 1994-1999, 1974
A;Title: The amino acid sequence of porcine parathyroid hormone.
A;Reference number: A90376; MUID:74253317; PMID:4840833
A;Accession: A90376
A;Molecule type: protein
A;Residues: 32-109 <SAU>
R;Brewer Jr., H.B.; Fairwell, T.; Rittel, W.; Littledike, T.; Arnaud, C.D.
Am. J. Med. 56, 759-766, 1974
A;Title: Recent studies on the chemistry of human, bovine and porcine parathyroid hor
A;Reference number: A90030; MUID:74173303; PMID:4598526
A;Contents: annotation
C;Superfamily: parathyroid hormone; parathyroid hormone homology
C;Keywords: calcium; hormone; parathyroid gland
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-31/Domain: propeptide #status experimental <PRO>
F;30-64/Domain: parathyroid hormone homology <PTH>
F;32-115/Product: parathyroid hormone #status experimental <MAT>

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Qy      1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
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Db     33 VSEIQLMHNLGKHLSSLERVEWLRKKLQDVHNFVALGASIVHRDGGSQRPRKKEDNVLVE 92

Qy     61 SHEKSLGEANKADVNVLTKAKSQ 83
          ||:||||||:|| |:|| ||| |
Db     93 SHQKSLGEADKAAVDVLIKAKPQ 115


RESULT 5
A05091
parathyroid hormone precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 16-Jul-1999
C;Accession: A05091; A26806
R;Heinrich, G.; Kronenberg, H.M.; Potts Jr., J.T.; Habener, J.F.
J. Biol. Chem. 259, 3320-3329, 1984
A;Reference number: A05091; MUID:84135846; PMID:6321505
A;Accession: A05091
A;Molecule type: DNA
A;Residues: 1-115 <HEI>
A;Cross-references: GB:K01268; NID:g206483; PIDN:AAA41979.1; PID:g206485
A;Note: the authors translated the codon GAA for residue 87 as Asp
R;Schmelzer, H.J.; Gross, G.; Widera, G.; Mayer, H.
Nucleic Acids Res. 15, 6740, 1987
A;Title: Nucleotide sequence of a full-length cDNA clone encoding preproparathyroid h
A;Reference number: A26806; MUID:87316938; PMID:3628009
A;Accession: A26806
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-115 <SCH>
A;Cross-references: GB:X05721; GB:Y00409; NID:g56002; PIDN:CAA29192.1; PID:g56003
C;Genetics:
A;Introns: 29/3
C;Superfamily: parathyroid hormone; parathyroid hormone homology
F;30-64/Domain: parathyroid hormone homology <PTH>

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Db         33 VSEIQLMHNLGKHLASVERMQWLRKKLQDVHNFVSLGVQMAAREGSYQRPTKKEENVLVD 92

Qy         61 SHEKSLGEANKADVNVLTKAKSQ 83
               : ||||| :||||:|| |||||
Db         93 GNSKSLGEGDKADVDVLVKAKSQ 115


RESULT 6
I51851
parathyroid hormone - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
C;Accession: I51851
R;Schmelzer, H.
Adv. Gene Technol. 21, 228-229, 1984
A;Title: Nucleotide sequence of cloned cDNA encoding rat prepro parathyroid hormone.
A;Reference number: I51851
A;Accession: I51851
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-105 <RES>
A;Cross-references: GB:M54875; NID:g601932; PIDN:AAA57156.1; PID:g601933
C;Genetics:
A;Gene: PTH
C;Superfamily: parathyroid hormone; parathyroid hormone homology
F;20-54/Domain: parathyroid hormone homology <PTH>

  Query Match             71.8%;  Score 303;  DB 2;  Length 105;
  Best Local Similarity   69.9%;  Pred. No. 5.2e-25;
  Matches   58;  Conservative   12;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
              :||||||||||||| |:||::|||||||| ||||:||  :| |:   ||| |||:||||:
Db         23 ISEIQLMHNLGKHLASVERMQWLRKKLQDGHNFVSLGVQMAAREGSYQRPTKKEENVLVD 82

Qy         61 SHEKSLGEANKADVNVLTKAKSQ 83
               : ||||| :||||:|| |||||
Db         83 GNSKSLGEGDKADVDVLVKAKSQ 105


RESULT 7
A34937
parathyroid hormone precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 16-Jul-1999
C;Accession: A34937; I50411
R;Russell, J.; Sherwood, L.M.
Mol. Endocrinol. 3, 325-331, 1989
A;Title: Nucleotide sequence of the DNA complementary to avian (chicken) preproparathyrc
A;Reference number: A34937; MUID:89219100; PMID:2710135
A;Accession: A34937
A;Molecule type: mRNA
A;Residues: 1-119 <RUS>
A;Cross-references: GB:M31604; NID:g212767; PIDN:AAA49093.1; PID:g212768
R;Khosla, S.; Demay, M.; Pines, M.; Hurwitz, S.; Potts, J.T.
J. Bone Miner. Res. 3, 689-698, 1988
A;Title: Nucleotide sequence of cloned cDNAs encoding chicken preproparathyroid hormone.
A;Reference number: I50411; MUID:89284968; PMID:3251402
A;Accession: I50411
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-119 <KHO>
A;Cross-references: GB:M36522; NID:g212591; PIDN:AAB02866.1; PID:g212592
C;Superfamily: parathyroid hormone; parathyroid hormone homology
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-31/Domain: propeptide #status predicted <PRO>
F;30-64/Domain: parathyroid hormone homology <PTH>
F;32-119/Product: parathyroid hormone #status predicted <MAT>

  Query Match             41.4%;  Score 174.5;  DB 2;  Length 119;
  Best Local Similarity   44.7%;  Pred. No. 2.3e-11;
  Matches   42;  Conservative   14;  Mismatches   17;  Indels   21;  Gaps    2;
```

```
Qy          1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
              |||:|||||||:| :::|| :||: ||||||:        |  || :|||| ||| || |
Db         33 VSEMQLMHNLGEHRHTVERQDWLQMKLQDVHS--------ALEDARTQRPRNKEDIVLGE 84

Qy         61 -------------SHEKSLGEANKADVNVLTKAK 81
                           : :|   : :|| :||| | |
Db         85 IRNRRLLPEHLRAAVQKKSIDLDKAYMNVLFKTK 118


RESULT 8
G89813
DNA polymerase III gamma and tau subunits [imported] - Staphylococcus aureus (strain
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: G89813
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; O
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K
 C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: G89813
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-565 <KUR>
A;Cross-references: GB:BA000018; PID:g13700368; PIDN:BAB41666.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A;Gene: dnaX
C;Superfamily: DNA-directed DNA polymerase III gamma chain

  Query Match             17.3%;  Score 73;  DB 2;  Length 565;
  Best Local Similarity   29.4%;  Pred. No. 7.1;
  Matches   20;  Conservative   15;  Mismatches   23;  Indels   10;  Gaps    2;

Qy         14 LNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRP----RKKEDNVLVESHEKSLGEA 69
              |  ||::|      |::    | |  :||    |::|    :| ::   ::   | | :|
Db        376 LQRMEQLE------QELKTLKAQGVSVAPAQKSSKKPARGIQKSKNAFSMQQIAKVLDKA 429

Qy         70 NKADVNVL 77
              ||||: :|
Db        430 NKADIKLL 437


RESULT 9
F72408
leucine-tRNA ligase (EC 6.1.1.4) - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 03-Jun-2002
C;Accession: F72408
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
 C.M.
Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: F72408
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-824 <ARN>
A;Cross-references: GB:AE001702; GB:AE000512; NID:g4980662; PIDN:AAD35261.1; PID:g498
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM0168
C;Superfamily: leucine-tRNA ligase
C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

  Query Match             17.2%;  Score 72.5;  DB 2;  Length 824;
  Best Local Similarity   23.3%;  Pred. No. 12;
  Matches   21;  Conservative   25;  Mismatches   25;  Indels   19;  Gaps    4;

Qy          4 IQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALG-APLAP-------RDAGSQRPRKKED 55
              ::|:::| ::|||: : || || |:::   : |  :| ||        | |:       |
```

```
Db    692 MELVNHLSQYLNSVPQEEWNRKLLREIVEKLTLALSPFAPHLAEEFWHDLGN-------D 744

Qy     56 NVLVE----SHEKSLGEANKADVNVLTKAK 81
          :::|:    |::    |  : :: :    |
Db    745 SLVVQQSWPSYDPKALEVEEVEIAIQINGK 774


RESULT 10
I58383
retinoblastoma binding protein 1, splice form I - human
N;Alternate names: retinoblastoma-associated protein 2 (misnomer)
N;Contains: retinoblastoma binding protein 1, splice form II
C;Species: Homo sapiens (man)
C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
C;Accession: I58383; I58390; I78883; S16953; B42997
R;Fattaey, A.R.; Helin, K.; Dembski, M.S.; Dyson, N.; Harlow, E.; Vuocolo, G.A.; Hanobik
Oncogene 8, 3149-3156, 1993
A;Title: Characterization of the retinoblastoma binding proteins RBP1 and RBP2.
A;Reference number: I58383; MUID:94020841; PMID:8414517
A;Accession: I58383
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1257 <FAT>
A;Cross-references: GB:S66427; NID:g435775; PIDN:AAB28543.1; PID:g435776
R;Otterson, G.A.; Kratzke, R.A.; Lin, A.Y.; Johnston, P.G.; Kaye, F.J.
Oncogene 8, 949-957, 1993
A;Title: Alternative splicing of the RBP1 gene clusters in an internal exon that encodes
A;Reference number: I58390; MUID:93205410; PMID:8455946
A;Accession: I58390
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 338-384,'V',386-617,'R',619-652,'V',654-778,'T',780-1257 <OTT1>
A;Cross-references: GB:S57153; NID:g298681; PIDN:AAB25833.1; PID:g298682
A;Accession: I78883
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 338-384,'V',386-617,'R',619-652,'V',654-778,'T',780-1120,1175-1257 <OTT2>
A;Cross-references: GB:S57160; NID:g298683; PIDN:AAB25834.1; PID:g298684
R;Defeo-Jones, D.; Huang, P.S.; Jones, R.E.; Haskell, K.M.; Vuocolo, G.A.; Hanobik, M.G.
Nature 352, 251-254, 1991
A;Title: Cloning of cDNAs for cellular proteins that bind to the retinoblastoma gene pro
A;Reference number: S16953; MUID:91312450; PMID:1857421
A;Accession: S16953
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 855-1177,'S',1179-1195,'SENIICL' <DEF>
R;Kaelin Jr., W.G.; Krek, W.; Sellers, W.R.; DeCaprio, J.A.; Ajchenbaum, F.; Fuchs, C.S.
Cell 70, 351-364, 1992
A;Title: Expression cloning of a cDNA encoding a retinoblastoma-binding protein with E2F
A;Reference number: A42997; MUID:92346721; PMID:1638635
A;Accession: B42997
A;Molecule type: mRNA
A;Residues: 'MMTMKL',510-617,'R',619-1257 <KAE>
A;Experimental source: Akata cells
A;Note: the cited GenBank accession number, M96577, is apparently a misprint and does no
A;Note: sequence extracted from NCBI backbone (NCBIN:110020, NCBIP:110022)
C;Genetics:
A;Gene: GDB:RBP1
A;Cross-references: GDB:120340; OMIM:180260
A;Map position: 3q21-3q22
C;Superfamily: human retinoblastoma binding protein 1
C;Keywords: alternative splicing
F;1-1257/Product: retinoblastoma binding protein 1, splice form I #status predicted <SF1
F;1-1120,1175-1257/Product: retinoblastoma binding protein 1, splice form II #status pre

  Query Match             17.1%;  Score 72;  DB 1;  Length 1257;
  Best Local Similarity   26.8%;  Pred. No. 23;
  Matches   19;  Conservative   21;  Mismatches   27;  Indels    4;  Gaps    2;

Qy     13 HLNSMERVEWLRKKLQDVHN-FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANK 71
          ::|| ||: :|::|||::   :::| : :|  |   :| :||:  |   ||  :   :
Db   1179 NMNSTERISFLQEKLQEIRKYYMSLKSEVATIDRRRKRLKKKDREV---SHAGASMSSAS 1235
```

```
Qy     72 ADVNVLTKAKS 82
          :|  :   : |
Db   1236 SDTGMSPSSSS 1246


RESULT 11
T44010
virion protein [imported] - human herpesvirus 6
C;Species: human herpesvirus 6
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C;Accession: T44010; T44197
R;Isegawa, Y.; Mukai, T.; Nakano, K.; Kagawa, M.; Chen, J.; Mori, Y.; Sunagawa, T.; K
J. Virol. 73, 8053-8063, 1999
A;Title: Comparison of the complete DNA sequences of human herpesvirus 6 variants A a
A;Reference number: Z22732; MUID:99412319; PMID:10482554
A;Accession: T44010
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-555 <ISE>
A;Cross-references: EMBL:AB021506; NID:g4995977; PIDN:BAA78271.1; PID:g4996038
A;Experimental source: strain HST; pop. variant B
R;Dominguez, G.; Dambaugh, T.R.; Stamey, F.R.; Dewhurst, S.; Inoue, N.; Pellett, P.E.
J. Virol. 73, 8040-8052, 1999
A;Title: Human herpesvirus 6B genome sequence: coding content and comparison with hum
A;Reference number: Z22734; MUID:99412318; PMID:10482553
A;Accession: T44197
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-555 <DOM>
A;Cross-references: EMBL:AF157706; PIDN:AAB06348.1
A;Experimental source: strain Z29; variant B
C;Genetics:
A;Gene: U50
C;Superfamily: varicella-zoster virus gene 34 protein

  Query Match             16.5%;  Score 69.5;  DB 2;  Length 555;
  Best Local Similarity   35.4%;  Pred. No. 16;
  Matches   23;  Conservative   10;  Mismatches   27;  Indels    5;  Gaps    2;

Qy     23 LRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEA----NKADVNVLT 78
          ||:|:   |    |   |       ||  :|: :||  || |:: :|    |  :||| |
Db     42 LREKIDQGHRDKLLRMRLKTELDALQRKMQKDSDVL-NSHLKAIEDALLFTNDGEVNVET 100

Qy     79 KAKSQ 83
          || :|
Db    101 KADTQ 105


RESULT 12
B70356
chromosome assembly protein homolog - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 02-Jun-2000
C;Accession: B70356
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;
V.
Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: B70356
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1156 <AQF>
A;Cross-references: GB:AE000699; NID:g2983238; PIDN:AAC06839.1; PID:g2983243; GB:AE00
A;Experimental source: strain VF5
C;Genetics:
A;Gene: xcpC
C;Superfamily: chromosome segregation protein SMC1

  Query Match             16.0%;  Score 67.5;  DB 2;  Length 1156;
  Best Local Similarity   29.0%;  Pred. No. 61;
  Matches   27;  Conservative   16;  Mismatches   25;  Indels   25;  Gaps    4;
```

```
Qy      1 VSEIQLMHNLGKHLNSMER--------VEWLRKKLQDVHNFVALGAPLAPRDAGSQRPR- 51
          ||||:      | || :||        :|:| |::|:             |:  ::| :
Db    794 VSEIE------KSLNEIERELNKKTYELEYLEKEIQEKER---------EREYLTERIKS 838

Qy     52 -KKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 83
           |||   |:   ||:| |  :|:| |    | :
Db    839 LKKEIENLILFKEKTLQEVKEAEVKVYDYIKQK 871


RESULT 13
E82046
proteinase HslVU, ATPase subunit HslU VC2674 [imported] - Vibrio cholerae (strain N16961
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: E82046
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: E82046
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-443 <HEI>
A;Cross-references: GB:AE004333; GB:AE003852; NID:g9657266; PIDN:AAF95815.1; GSPDB:GN001
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VC2674
A;Map position: 1
C;Superfamily: heat shock protein hslU; FtsH/SEC18/CDC48-type ATP-binding domain homolog

  Query Match             15.9%;  Score 67;  DB 2;  Length 443;
  Best Local Similarity   28.8%;  Pred. No. 23;
  Matches   19;  Conservative   16;  Mismatches   27;  Indels    4;  Gaps    2;

Qy     13 HLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSL--GEAN 70
          |  :||:|::  ::| :     ||  |  ||||  |  :|:|::   :   | |  |: |
Db    112 HQQAMEKVKFRAEELAEERVLDALLPP--PRDAWGQAEQKEENSSTRQVFRKKLREGQLN 169

Qy     71 KADVNV 76
            :: :
Db    170 DKEIEI 175


RESULT 14
C71438
hypothetical protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
A;Variety: columbia
C;Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 20-Jun-2000
C;Accession: C71438
R;Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk
 P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenegger, T.; Pohl, T.M.; Terryn, N.; Giel
avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.
Nature 391, 485-488, 1998
A;Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech
erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ans
C.; Chalwatzis, N.
A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thal
A;Reference number: A71400; MUID:98121113; PMID:9461215
A;Accession: C71438
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-655 <BEV>
A;Cross-references: GB:Z97342; NID:g2245031; PID:g2245056
C;Genetics:
A;Map position: 4COP9-4G3845

  Query Match             15.9%;  Score 67;  DB 2;  Length 655;
  Best Local Similarity   24.3%;  Pred. No. 36;
  Matches   18;  Conservative   21;  Mismatches   31;  Indels    4;  Gaps    2;
```

```
Qy     12 KHLNSMER-VEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKK---EDNVLVESHEKSLG 67
          | ::  :: |  |:|:::   : |    || | |:       |   :: :|||:  : |
Db    252 KQIDQKDKGVSTLKKRVKKKEDPVPSSDPLKPYDSNGMEVEDKTSRDEELLVENKSEELS 311

Qy     68 EANKADVNVLTKAK 81
          : :||::|   :|:
Db    312 DTSKANMNNQLQAR 325


RESULT 15
B71438
hypothetical protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
A;Variety: columbia
C;Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 20-Jun-2000
C;Accession: B71438
R;Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; D
 P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenegger, T.; Pohl, T.M.; Terryn, N.; G
avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B
Nature 391, 485-488, 1998
A;Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomen
erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.;
C.; Chalwatzis, N.
A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis t
A;Reference number: A71400; MUID:98121113; PMID:9461215
A;Accession: B71438
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-674 <BEV>
A;Cross-references: GB:Z97342; NID:g2245031; PID:g2245057
C;Genetics:
A;Map position: 4COP9-4G3845

  Query Match             15.9%;  Score 67;  DB 2;  Length 674;
  Best Local Similarity   24.3%;  Pred. No. 37;
  Matches   18;  Conservative   21;  Mismatches   31;  Indels    4;  Gaps    2;

Qy     12 KHLNSMER-VEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKK---EDNVLVESHEKSLG 67
          | ::  :: |  |:|:::   : |    || | |:       |   :: :|||:  : |
Db    271 KQIDQKDKGVSTLKKRVKKKEDPVPSSDPLKPYDSNGMEVEDKTSRDEELLVENKSEELS 330

Qy     68 EANKADVNVLTKAK 81
          : :||::|   :|:
Db    331 DTSKANMNNQLQAR 344


Search completed: March 13, 2003, 15:02:25
Job time : 19.1045 secs
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                    GenCore version 5.1.4_p5_4578
           Copyright (c) 1993 - 2003  Compugen Ltd.


OM protein - protein search, using sw model

Run on:         March 13, 2003, 14:52:59 ; Search time 9.29105 Seconds
                                           (without alignments)
                                           370.522 Million cell updates/sec

Title:          US-09-636-530-2
Perfect score:  422
Sequence:       1 VSEIQLMHNLGKHLNSMERV..........KSLGEANKADVNVLTKAKSQ 83

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters:      112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       SwissProt_40:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                    SUMMARIES
                   %
Result           Query
  No.    Score   Match Length DB  ID                         Description
--------------------------------------------------------------------------------
    1      417    98.8    115  1  PTHY_HUMAN                 P01270 homo sapien
    2      410    97.2    115  1  PTH_MACFA                  Q9xt35 macaca fasc
    3      366    86.7    115  1  PTHY_CANFA                 P52212 canis famil
    4      359    85.1    115  1  PTHY_BOVIN                 P01268 bos taurus
    5      355    84.1    115  1  PTHY_PIG                   P01269 sus scrofa
    6      311    73.7    115  1  PTHY_RAT                   P04089 rattus norv
    7    174.5    41.4    119  1  PTHY_CHICK                 P15743 gallus gall
    8     72.5    17.2    824  1  SYL_THEMA                  Q9wy15 thermotoga
    9       72    17.1   1257  1  RBB1_HUMAN                 P29374 homo sapien
   10     69.5    16.5    555  1  UL25_HSV6Z                 P52537 human herpe
   11       67    15.9    443  1  HSLU_VIBCH                 Q9knq7 vibrio chol
   12     66.5    15.8    378  1  UL25_HSV6G                 P52536 human herpe
   13     66.5    15.8    555  1  UL25_HSV6U                 P52387 human herpe
   14       65    15.4   1244  1  MIX1_CAEEL                 Q09591 caenorhabdi
   15     64.5    15.3    205  1  KGUA_CHLPN                 Q9z961 chlamydia p
   16       64    15.2    642  1  FLID_CAMJE                 Q9phw6 campylobact
   17     63.5    15.0   1270  1  ITN1_XENLA                 O42287 xenopus lae
   18       63    14.9    992  1  FLT3_MOUSE                 Q00342 mus musculu
   19       63    14.9   1033  1  Y328_MYCPN                 P75310 mycoplasma
   20       63    14.9   1388  1  RPOD_TOBAC                 P38550 nicotiana t
   21       63    14.9   1937  1  MYH8_HUMAN                 P13535 homo sapien
   22     62.5    14.8    370  1  YA44_HELPY                 O25685 helicobacte
   23     62.5    14.8    632  1  DNAK_ACTAC                 P71331 actinobacil
   24     62.5    14.8   1658  1  ITN2_MOUSE                 Q9z0r6 mus musculu
   25       62    14.7    300  1  YBDO_ECOLI                 P77746 escherichia
   26       62    14.7   1041  1  DD16_HUMAN                 O60231 homo sapien
   27     61.5    14.6    282  1  VIT4_CAEEL                 P18947 caenorhabdi
   28     61.5    14.6    366  1  YE05_HAEIN                 P44180 haemophilus
   29       61    14.5    429  1  DPD2_ORYSA                 Q9lre5 oryza sativ
   30       61    14.5    910  1  HUL5_YEAST                 P53119 saccharomyc
   31     60.5    14.3    942  1  PKL1_HUMAN                 Q16512 homo sapien
   32     60.5    14.3   1721  1  ITN1_HUMAN                 Q15811 homo sapien
   33       60    14.2    455  1  HYIN_PSESS                 P06618 pseudomonas
   34       60    14.2    668  1  DCRA_DESVH                 P35841 desulfovibr
   35       60    14.2   1027  1  KINN_MOUSE                 P33175 mus musculu
   36       60    14.2   1032  1  KINN_HUMAN                 Q12840 homo sapien
   37       60    14.2   1084  1  MYSS_RABIT                 P02562 oryctolagus
   38       60    14.2   1172  1  SYK2_MYCTU                 P94974 mycobacteri
   39       60    14.2   1935  1  MYSS_CYPCA                 Q90339 cyprinus ca
   40       60    14.2   1938  1  MYH4_RABIT                 Q28641 oryctolagus
   41       60    14.2   1940  1  MYH3_CHICK                 P02565 gallus gall
   42       60    14.2   2390  1  SPCP_HUMAN                 O15020 homo sapien
   43     59.5    14.1    437  1  MURC_STAAU                 O31211 staphylococ
   44     59.5    14.1   1154  1  KDGD_MESAU                 Q64398 mesocricetu
   45       59    14.0    177  1  PTHR_HUMAN                 P12272 homo sapien


                                   ALIGNMENTS


RESULT 1
PTHY_HUMAN
ID   PTHY_HUMAN     STANDARD;      PRT;   115 AA.
AC   P01270;
DT   21-JUL-1986 (Rel. 01, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Parathyroid hormone precursor (Parathyrin) (PTH) (Parathormone).
GN   PTH.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=82150870; PubMed=6950381;
RA   Hendy G.N., Kronenberg H.M., Potts J.T. Jr., Rich A.;
RT   "Nucleotide sequence of cloned cDNAs encoding human preproparathyroid
RT   hormone.";
RL   Proc. Natl. Acad. Sci. U.S.A. 78:7365-7369(1981).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83169834; PubMed=6220408;
RA   Vasicek T.J., McCevitt B.E., Freeman M.W., Fennick B.J.,
RA   Hendy G.N., Potts J.T. Jr., Rich A., Kronenberg H.M.;
RT   "Nucleotide sequence of the human parathyroid hormone gene.";
RL   Proc. Natl. Acad. Sci. U.S.A. 80:2127-2131(1983).
RN   [3]
RP   SEQUENCE OF 26-37.
RX   MEDLINE=74174967; PubMed=4833516;
RA   Jacobs J.W., Kemper B., Niall H.D., Habener J.F., Potts J.T. Jr.;
RT   "Structural analysis of human proparathyroid hormone by a new
RT   microsequencing approach.";
RL   Nature 249:155-157(1974).
RN   [4]
RP   SEQUENCE OF 32-68.
RX   MEDLINE=74111656; PubMed=4521809;
RA   Niall H.D., Sauer R.T., Jacobs J.W., Keutmann H.T., Segre G.V.,
RA   O'Riordan J.L.H., Aurbach G.D., Potts J.T. Jr.;
RT   "The amino-acid sequence of the amino-terminal 37 residues of human
RT   parathyroid hormone.";
RL   Proc. Natl. Acad. Sci. U.S.A. 71:384-388(1974).
RN   [5]
RP   SEQUENCE OF 61-83 AND 84-115.
RX   MEDLINE=79082855; PubMed=728431;
RA   Keutmann H.T., Sauer M.M., Hendy G.N., O'Riordan J.L.H.,
RA   Potts J.T. Jr.;
RT   "Complete amino acid sequence of human parathyroid hormone.";
RL   Biochemistry 17:5723-5729(1978).
RN   [6]
RP   SEQUENCE OF 75-100.
RA   Keutmann H.T., Niall H.D., Jacobs J.W., Barling P.M., Hendy G.N.,
RA   O'Riordan J.L.H., Potts J.T. Jr.;
RL   (In) Talmadge R.V., Owen M., Parsons J.A. (eds.);
RL   Calcium-regulating hormones, pp.9-14, Excerpta Medica Foundation,
RL   Amsterdam (1975).
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RN   [7]
RP   REVISIONS.
RX   MEDLINE=75146516; PubMed=1125201;
RA   Keutmann H.T., Niall H.D., O'Riordan J.L.H., Potts J.T. Jr.;
RT   "A reinvestigation of the amino-terminal sequence of human
RT   parathyroid hormone.";
RL   Biochemistry 14:1842-1847(1975).
RN   [8]
RP   SYNTHESIS OF 32-65.
RX   MEDLINE=75059220; PubMed=4474131;
RA   Tregear G.W., van Rietschoten J., Green E., Niall H.D.,
RA   Keutmann H.T., Parsons J.A., O'Riordan J.L.H., Potts J.T. Jr.;
RT   "Solid-phase synthesis of the biologically active N-terminal 1-34
RT   peptide of human parathyroid hormone.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 355:415-421(1974).
RN   [9]
RP   SYNTHESIS OF 32-65.
RX   MEDLINE=73227467; PubMed=4721748;
RA   Andreatta R.H., Hartmann A., Joehl A., Kamber B., Maier R.,
RA   Riniker B., Rittel W., Sieber P.;
RT   "Synthesis of sequence 1-34 of human parathyroid hormone.";
RL   Helv. Chim. Acta 56:470-473(1973).
RN   [10]
RP   STRUCTURE BY NMR OF 32-65.
RX   MEDLINE=91299748; PubMed=2069952;
RA   Klaus W., Dieckmann T., Wray V., Schomburg D., Wingender E., Mayer H.;
RT   "Investigation of the solution structure of the human parathyroid
RT   hormone fragment (1-34) by 1H NMR spectroscopy, distance geometry,
RT   and molecular dynamics calculations.";
RL   Biochemistry 30:6936-6942(1991).
RN   [11]
RP   STRUCTURE BY NMR OF 32-65.
RX   MEDLINE=93345518; PubMed=8344299;
RA   Barden J.A., Cuthbertson R.M.;
RT   "Stabilized NMR structure of human parathyroid hormone(1-34).";
RL   Eur. J. Biochem. 215:315-321(1993).
RN   [12]
RP   STRUCTURE BY NMR OF 32-68.
RX   MEDLINE=95318084; PubMed=7797503;
RA   Marx U.C., Austermann S., Bayer P., Adermann K., Ejchart A.,
RA   Sticht H., Walter S., Schmid F.-X., Jaenicke R., Forssmann W.-G.,
RA   Roesch P.;
RT   "Structure of human parathyroid hormone 1-37 in solution.";
RL   J. Biol. Chem. 270:15194-15202(1995).
RN   [13]
RP   STRUCTURE BY NMR OF 32-70.
RX   MEDLINE=20090619; PubMed=10623601;
RA   Marx U.C., Adermann K., Bayer P., Forssmann W.-G., Rosch P.;
RT   "Solution structures of human parathyroid hormone fragments
RT   hPTH(1-34) and hPTH(1-39) and bovine parathyroid hormone fragment
RT   bPTH(1-37).";
RL   Biochem. Biophys. Res. Commun. 267:213-220(2000).
RN   [14]
RP   VARIANT ARG-18.
RX   MEDLINE=91009811; PubMed=2212001;
RA   Arnold A., Horst S.A., Gardella T.J., Baba H., Levine M.A.,
RA   Kronenberg H.M.;
RT   "Mutation of the signal peptide-encoding region of the
RT   preproparathyroid hormone gene in familial isolated
RT   hypoparathyroidism.";
RL   J. Clin. Invest. 86:1084-1087(1990).
CC   -!- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC       BONE AND PREVENTING THEIR RENAL EXCRETION.
CC   -!- DISEASE: DEFECTS IN PTH ARE A CAUSE OF FAMILIAL ISOLATED
CC       HYPOPARATHYROIDISM (FIH).
CC   -!- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
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CC   --------------------------------------------------------------------------
DR   EMBL; J00301; AAA60215.1; -.
DR   EMBL; V00597; CAA23843.1; -.
DR   EMBL; A29146; CAA01956.1; -.
DR   PIR; A01536; PTHU.
DR   PIR; A19339; A19339.
DR   PDB; 1HPH; 10-JUL-95.
DR   PDB; 1HTH; 15-OCT-97.
DR   PDB; 1ZWA; 12-MAR-97.
DR   PDB; 1ZWB; 12-MAR-97.
DR   PDB; 1ZWD; 12-MAR-97.
DR   PDB; 1ZWE; 12-MAR-97.
DR   PDB; 1ZWF; 16-JUN-97.
DR   PDB; 1ZWG; 16-JUN-97.
DR   PDB; 1BWX; 14-JAN-00.
DR   PDB; 1HPY; 14-JAN-00.
DR   Genew; HGNC:9606; PTH.
DR   MIM; 146200; -.
DR   MIM; 168450; -.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   Pfam; PF01279; Parathyroid; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   SMART; SM00087; PTH; 1.
DR   PROSITE; PS00335; PARATHYROID; 1.
KW   Hormone; Signal; Disease mutation; 3D-structure.
FT   SIGNAL        1     25
FT   PROPEP       26     31
FT   CHAIN        32    115       PARATHYROID HORMONE.
FT   VARIANT      18     18       C -> R (IN FIH; LEADS TO INEFFICIENT
FT                                PROCESSING OF THE PRECURSOR).
FT                                /FTId=VAR_006047.
FT   CONFLICT    107    107       N -> D (IN REF. 5).
SQ   SEQUENCE   115 AA;  12861 MW;  849015736A6E5597 CRC64;

  Query Match             98.8%;  Score 417;  DB 1;  Length 115;
  Best Local Similarity   98.8%;  Pred. No. 1.8e-39;
  Matches   82;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       33 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 92

Qy       61 SHEKSLGEANKADVNVLTKAKSQ 83
              |||||||||:|||||||||||||
Db       93 SHEKSLGEADKADVNVLTKAKSQ 115


RESULT 2
PTH_MACFA
ID   PTH_MACFA      STANDARD;      PRT;   115 AA.
AC   Q9XT35;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Parathyroid hormone precursor (Parathyrin) (PTH).
GN   PTH.
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Malaivijitnond S., Takenaka O.;
RT   "Nucleotide sequences of parathyroid gene in five species of macaque
RT   of Thailand.";
RL   J. Sci. Res. Chulalongkorn Univ. 23:135-142(1998).
CC   -!- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC       BONE AND PREVENTING THEIR RENAL EXCRETION.
CC   -!- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
CC   --------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; AF130257; AAD42777.1; -.
DR   HSSP; P01270; 1HPY.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   Pfam; PF01279; Parathyroid; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   SMART; SM00087; PTH; 1.
DR   PROSITE; PS00335; PARATHYROID; 1.
KW   Hormone; Signal.
FT   SIGNAL        1     25       BY SIMILARITY.
FT   PROPEP       26     31       BY SIMILARITY.
FT   CHAIN        32    115       PARATHYROID HORMONE.
SQ   SEQUENCE   115 AA;  12890 MW;  8C2500EF24BE5597 CRC64;

  Query Match             97.2%;  Score 410;  DB 1;  Length 115;
  Best Local Similarity   95.2%;  Pred. No. 1.1e-38;
  Matches   79;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
          |||||||||||||||||||||||||||||||||:||||||||||||||||||||||:|||
Db     33 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFIALGAPLAPRDAGSQRPRKKEDNILVE 92

Qy     61 SHEKSLGEANKADVNVLTKAKSQ 83
          |||||||||:||||:||||||||
Db     93 SHEKSLGEADKADVDVLTKAKSQ 115


RESULT 3
PTHY_CANFA
ID   PTHY_CANFA     STANDARD;      PRT;   115 AA.
AC   P52212;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   Parathyroid hormone precursor (Parathyrin) (PTH).
GN   PTH.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Parathyroid;
RX   MEDLINE=95369696; PubMed=7642102;
RA   Rosol T.J., Steinmeyer C.L., McCauley L.K., Groene A.,
RA   DeWille J.W., Capen C.C.;
RT   "Sequences of the cDNAs encoding canine parathyroid hormone-related
RT   protein and parathyroid hormone.";
RL   Gene 160:241-243(1995).
CC   -!- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC       BONE AND PREVENTING THEIR RENAL EXCRETION.
CC   -!- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
CC   --------------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; U15662; AAA82584.1; -.
DR   HSSP; P01268; 1ZWC.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003625; Pthyrhorm_sub.
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DR   Pfam; PF01279; Parathyroid; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   SMART; SM00087; PTH; 1.
DR   PROSITE; PS00335; PARATHYROID; 1.
KW   Hormone; Signal.
FT   SIGNAL        1     25       BY SIMILARITY.
FT   PROPEP       26     31       BY SIMILARITY.
FT   CHAIN        32    115       PARATHYROID HORMONE.
SQ   SEQUENCE   115 AA;  12957 MW;  FC38F77F1C8CFE56 CRC64;

  Query Match             86.7%;  Score 366;  DB 1;  Length 115;
  Best Local Similarity   86.7%;  Pred. No. 8.1e-34;
  Matches   72;  Conservative    6;  Mismatches    5;  Indels    0;  Gaps    0;

Qy      1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
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Db     33 VSEIQFMHNLGKHLSSMERVEWLRKKLQDVHNFVALGAPIAHRDGSSQRPLKKEDNVLVE 92

Qy     61 SHEKSLGEANKADVNVLTKAKSQ 83
          |::||||||:||||:||||||||
Db     93 SYQKSLGEADKADVDVLTKAKSQ 115


RESULT 4
PTHY_BOVIN
ID   PTHY_BOVIN     STANDARD;      PRT;   115 AA.
AC   P01268;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Parathyroid hormone precursor (Parathyrin) (PTH).
GN   PTH.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=80056617; PubMed=388425;
RA   Kronenberg H.M., McDevitt B.E., Majzoub J.A., Nathans J., Sharp P.A.,
RA   Potts J.T. Jr., Rich A.;
RT   "Cloning and nucleotide sequence of DNA coding for bovine
RT   preproparathyroid hormone.";
RL   Proc. Natl. Acad. Sci. U.S.A. 76:4981-4985(1979).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=82037785; PubMed=6170060;
RA   Weaver C.A., Gordon D.F., Kemper B.;
RT   "Introduction by molecular cloning of artifactual inverted sequences
RT   at the 5' terminus of the sense strand of bovine parathyroid hormone
RT   cDNA.";
RL   Proc. Natl. Acad. Sci. U.S.A. 78:4073-4077(1981).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83105964; PubMed=6185374;
RA   Weaver C.A., Gordon D.F., Kemper B.;
RT   "Nucleotide sequence of bovine parathyroid hormone messenger RNA.";
RL   Mol. Cell. Endocrinol. 28:411-424(1982).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=84262483; PubMed=6086460;
RA   Weaver C.A., Gordon D.F., Kissil M.S., Mead D.A., Kemper B.;
RT   "Isolation and complete nucleotide sequence of the gene for bovine
RT   parathyroid hormone.";
RL   Gene 28:319-329(1984).
RN   [5]
RP   SEQUENCE OF 26-115.
RX   MEDLINE=74142666; PubMed=4522780;
RA   Hamilton J.W., Niall H.D., Jacobs J.W., Keutmann H.T., Potts J.T. Jr.,
RA   Cohn D.V.;
RT   "The N-terminal amino-acid sequence of bovine proparathyroid
RT   hormone.";
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RL   Proc. Natl. Acad. Sci. U.S.A. 71:653-656(1974).
RN   [6]
RP   SEQUENCE OF 32-115.
RX   MEDLINE=71076162; PubMed=5531031;
RA   Niall H.D., Keutmann H.T., Sauer R., Hogan M.L., Dawson B.F.,
RA   Aurbach G.D., Potts J.T. Jr.;
RT   "The amino acid sequence of bovine parathyroid hormone I.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 351:1586-1588(1970).
RN   [7]
RP   SEQUENCE OF 32-115.
RX   MEDLINE=71063634; PubMed=5275384;
RA   Brewer H.B. Jr., Ronan R.;
RT   "Bovine parathyroid hormone: amino acid sequence.";
RL   Proc. Natl. Acad. Sci. U.S.A. 67:1862-1869(1970).
RN   [8]
RP   SYNTHESIS OF 32-65.
RX   MEDLINE=71091588; PubMed=4322265;
RA   Potts J.T. Jr., Tregear G.W., Keutmann H.T., Niall H.D., Sauer R.,
RA   Deftos L.J., Dawson B.F., Hogan M.L., Aurbach G.D.;
RT   "Synthesis of a biologically active N-terminal tetratriacontapeptide
RT   of parathyroid hormone.";
RL   Proc. Natl. Acad. Sci. U.S.A. 68:63-67(1971).
RN   [9]
RP   STRUCTURE BY NMR OF 32-68.
RX   MEDLINE=20090619; PubMed=10623601;
RA   Marx U.C., Adermann K., Bayer P., Forssmann W.-G., Rosch P.;
RT   "Solution structures of human parathyroid hormone fragments
RT   hPTH(1-34) and hPTH(1-39) and bovine parathyroid hormone fragment
RT   bPTH(1-37).";
RL   Biochem. Biophys. Res. Commun. 267:213-220(2000).
CC   -!- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC       BONE AND PREVENTING THEIR RENAL EXCRETION.
CC   -!- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
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CC   --------------------------------------------------------------------------
DR   EMBL; V00106; CAA23439.1; -.
DR   EMBL; J00024; AAA30747.1; -.
DR   EMBL; K01938; AAA30749.1; -.
DR   EMBL; M25082; AAA30748.1; -.
DR   PIR; A01534; PTBO.
DR   PIR; A24949; A24949.
DR   PDB; 1ZWC; 12-MAR-97.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   Pfam; PF01279; Parathyroid; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   SMART; SM00087; PTH; 1.
DR   PROSITE; PS00335; PARATHYROID; 1.
KW   Hormone; Signal; 3D-structure.
FT   SIGNAL        1     25
FT   PROPEP       26     31
FT   CHAIN        32    115       PARATHYROID HORMONE.
FT   CONFLICT    106    106       V -> G (IN REF. 4).
SQ   SEQUENCE   115 AA;  12980 MW;  2ED246B348880710 CRC64;

  Query Match             85.1%;  Score 359;  DB 1;  Length 115;
  Best Local Similarity   85.5%;  Pred. No. 4.8e-33;
  Matches   71;  Conservative    5;  Mismatches    7;  Indels    0;  Gaps    0;

Qy      1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
          ||||| ||||||||:||||||||||||||||||||||| :| ||  ||||||||||||||
Db     33 VSEIQFMHNLGKHLSSMERVEWLRKKLQDVHNFVALGASIAYRDGSSQRPRKKEDNVLVE 92

Qy     61 SHEKSLGEANKADVNVLTKAKSQ 83
          ||:||||||:||||:|| ||| |
Db     93 SHQKSLGEADKADVDVLIKAKPQ 115
```

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RESULT 5
PTHY_PIG
ID   PTHY_PIG       STANDARD;      PRT;   115 AA.
AC   P01269;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   Parathyroid hormone precursor (Parathyrin) (PTH).
GN   PTH.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87316938; PubMed=3628009;
RA   Schmelzer H.-J., Gross G., Widera G., Mayer H.;
RT   "Nucleotide sequence of a full-length cDNA clone encoding
RT   preproparathyroid hormone from pig and rat.";
RL   Nucleic Acids Res. 15:6740-6740(1987).
RN   [2]
RP   SEQUENCE OF 26-115.
RX   MEDLINE=76018954; PubMed=1164500;
RA   Chu L.L.H., Huang W.-Y., Littledike E.T., Hamilton J.W., Cohn D.V.;
RT   "Porcine proparathyroid hormone. Identification, biosynthesis, and
RT   partial amino acid sequence.";
RL   Biochemistry 14:3631-3635(1975).
RN   [3]
RP   SEQUENCE OF 32-115.
RX   MEDLINE=74253317; PubMed=4840833;
RA   Sauer R.T., Niall H.D., Hogan M.L., Keutmann H.T., O'Riordan J.L.H.,
RA   Potts J.T. Jr.;
RT   "The amino acid sequence of porcine parathyroid hormone.";
RL   Biochemistry 13:1994-1999(1974).
CC   -!- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC       BONE AND PREVENTING THEIR RENAL EXCRETION.
CC   -!- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
CC   --------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; X05722; CAA29193.1; -.
DR   PIR; A01535; PTPG.
DR   PIR; B26806; B26806.
DR   HSSP; P01270; 1BWX.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   Pfam; PF01279; Parathyroid; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   SMART; SM00087; PTH; 1.
DR   PROSITE; PS00335; PARATHYROID; 1.
KW   Hormone; Signal.
FT   SIGNAL        1     25
FT   PROPEP       26     31
FT   CHAIN        32    115       PARATHYROID HORMONE.
SQ   SEQUENCE   115 AA;  12852 MW;  9FE8BCDE614BAC16 CRC64;

  Query Match             84.1%;  Score 355;  DB 1;  Length 115;
  Best Local Similarity   84.3%;  Pred. No. 1.3e-32;
  Matches   70;  Conservative    6;  Mismatches    7;  Indels    0;  Gaps    0;

Qy      1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
          ||||||||||||||:|:||||||||||||||||||||| :  || |||||||||||||||
Db     33 VSEIQLMHNLGKHLSSLERVEWLRKKLQDVHNFVALGASIVHRDGGSQRPRKKEDNVLVE 92

Qy     61 SHEKSLGEANKADVNVLTKAKSQ 83
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              ||:||||||:|| |:|| ||| |
Db         93 SHQKSLGEADKAAVDVLIKAKPQ 115


RESULT 6
PTHY_RAT
ID   PTHY_RAT       STANDARD;      PRT;   115 AA.
AC   P04089; Q63473;
DT   01-NOV-1986 (Rel. 03, Created)
DT   01-NOV-1986 (Rel. 03, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Parathyroid hormone precursor (Parathyrin) (PTH).
GN   PTH.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=84135846; PubMed=6321505;
RA   Heinrich G., Kronenberg H.M., Potts J.T. Jr., Habener J.F.;
RT   "Gene encoding parathyroid hormone. Nucleotide sequence of the rat
RT   gene and deduced amino acid sequence of rat preproparathyroid
RT   hormone.";
RL   J. Biol. Chem. 259:3320-3329(1984).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87316938; PubMed=3628009;
RA   Schmelzer H.-J., Gross G., Widera G., Mayer H.;
RT   "Nucleotide sequence of a full-length cDNA clone encoding
RT   preproparathyroid hormone from pig and rat.";
RL   Nucleic Acids Res. 15:6740-6740(1987).
RN   [3]
RP   SEQUENCE OF 10-115 FROM N.A.
RC   TISSUE=Parathyroid;
RA   Schmelzer H.J., Gross G., Mayer H.;
RT   "Nucleotide sequence of cloned cDNA encoding rat prepro parathyroid
RT   hormone.";
RL   Adv. Gene Technol. 21:228-229(1984).
RN   [4]
RP   SEQUENCE OF 32-115 FROM N.A.
RC   STRAIN=Sprague-Dawley; TISSUE=Brain, Parathyroid, and Liver;
RX   MEDLINE=96079910; PubMed=7588314;
RA   Nutley M.T., Parimi S.A., Harvey S.;
RT   "Sequence analysis of hypothalamic parathyroid hormone messenger
RT   ribonucleic acid.";
RL   Endocrinology 136:5600-5607(1995).
CC   -!- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC       BONE AND PREVENTING THEIR RENAL EXCRETION.
CC   -!- TISSUE SPECIFICITY: HYPOTHALAMUS AND PARATHYROID GLAND.
CC   -!- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
CC   --------------------------------------------------------------------------
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CC   --------------------------------------------------------------------------
DR   EMBL; K01268; AAA41979.1; -.
DR   EMBL; X05721; CAA29192.1; -.
DR   EMBL; M54875; AAA57156.1; -.
DR   EMBL; S80127; -; NOT_ANNOTATED_CDS.
DR   PIR; A05091; A05091.
DR   PIR; A26806; A26806.
DR   HSSP; P01270; 1ZWB.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   Pfam; PF01279; Parathyroid; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   SMART; SM00087; PTH; 1.
DR   PROSITE; PS00335; PARATHYROID; 1.
KW   Hormone; Signal.
FT   SIGNAL        1     25
FT   PROPEP       26     31
FT   CHAIN        32    115       PARATHYROID HORMONE.
FT   CONFLICT     18     18       C -> Y (IN REF. 3).
FT   CONFLICT     23     23       A -> T (IN REF. 3).
FT   CONFLICT     33     33       V -> I (IN REF. 3).
FT   CONFLICT     62     62       V -> G (IN REF. 3).
SQ   SEQUENCE   115 AA;  12722 MW;  7B434CFCA528B230 CRC64;

  Query Match             73.7%;  Score 311;  DB 1;  Length 115;
  Best Local Similarity   72.3%;  Pred. No. 1e-27;
  Matches   60;  Conservative   11;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
              |||||||||||||| |:||::|||||||||||||:||  :| |:   ||| |||:||||:
Db         33 VSEIQLMHNLGKHLASVERMQWLRKKLQDVHNFVSLGVQMAAREGSYQRPTKKEENVLVD 92

Qy         61 SHEKSLGEANKADVNVLTKAKSQ 83
              :  ||||| :||||:|| |||||
Db         93 GNSKSLGEGDKADVDVLVKAKSQ 115


RESULT 7
PTHY_CHICK
ID   PTHY_CHICK     STANDARD;      PRT;   119 AA.
AC   P15743;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-APR-1990 (Rel. 14, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   Parathyroid hormone precursor (PTH).
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89219100; PubMed=2710135;
RA   Russell J., Sherwood L.M.;
RT   "Nucleotide sequence of the DNA complementary to avian (chicken)
RT   preproparathyroid hormone mRNA and the deduced sequence of the
RT   hormone precursor.";
RL   Mol. Endocrinol. 3:325-331(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89284968; PubMed=3251402;
RA   Khosla S., Demay M., Pines M., Hurwitz S., Potts J.T. Jr.,
RA   Kronenberg H.M.;
RT   "Nucleotide sequence of cloned cDNAs encoding chicken
RT   preproparathyroid hormone.";
RL   J. Bone Miner. Res. 3:689-698(1988).
CC   -!- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC       BONE AND PREVENTING THEIR RENAL EXCRETION.
CC   -!- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
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CC   --------------------------------------------------------------------------
DR   EMBL; M31604; AAA49093.1; -.
DR   EMBL; M36522; AAB02866.1; -.
DR   PIR; A34937; A34937.
DR   HSSP; P01270; 1HPY.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   Pfam; PF01279; Parathyroid; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   SMART; SM00087; PTH; 1.
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DR   PROSITE; PS00335; PARATHYROID; 1.
KW   Hormone; Signal.
FT   SIGNAL        1     25
FT   PROPEP       26     31
FT   CHAIN        32    119       PARATHYROID HORMONE.
SQ   SEQUENCE   119 AA;  13943 MW;  B309D8E772997F6E CRC64;

  Query Match             41.4%;  Score 174.5;  DB 1;  Length 119;
  Best Local Similarity   44.7%;  Pred. No. 1.4e-12;
  Matches   42;  Conservative   14;  Mismatches   17;  Indels   21;  Gaps    2;

Qy      1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
          |||:|||||||:| :::|| :||: ||||||:        |  || :|||| ||| || |
Db     33 VSEMQLMHNLGEHRHTVERQDWLQMKLQDVHS--------ALEDARTQRPRNKEDIVLGE 84

Qy     61 -------------SHEKSLGEANKADVNVLTKAK 81
                       : :|   : :|| :||| | |
Db     85 IRNRRLLPEHLRAAVQKKSIDLDKAYMNVLFKTK 118


RESULT 8
SYL_THEMA
ID   SYL_THEMA      STANDARD;      PRT;   824 AA.
AC   Q9WY15;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Leucyl-tRNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (LeuRS).
GN   LEUS OR TM0168.
OS   Thermotoga maritima.
OC   Bacteria; Thermotogae; Thermotogae (class); Thermotogales;
OC   Thermotogaceae; Thermotoga.
OX   NCBI_TaxID=2336;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MSB8 / DSM 3109;
RX   MEDLINE=99287316; PubMed=10360571;
RA   Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
RA   Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA   McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA   Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA   Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA   Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT   "Evidence for lateral gene transfer between Archaea and Bacteria from
RT   genome sequence of Thermotoga maritima.";
RL   Nature 399:323-329(1999).
CC   -!- CATALYTIC ACTIVITY: ATP + L-leucine + tRNA(Leu) = AMP +
CC       diphosphate + L-leucyl-tRNA(Leu).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
CC   --------------------------------------------------------------------------
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CC   --------------------------------------------------------------------------
DR   EMBL; AE001702; AAD35261.1; -.
DR   TIGR; TM0168; -.
DR   InterPro; IPR002302; Leu-tRNAsyntla.
DR   InterPro; IPR002300; tRNA-synt_1a.
DR   InterPro; IPR001412; tRNA-synt_I.
DR   Pfam; PF00133; tRNA-synt_1; 1.
DR   PRINTS; PR00985; TRNASYNTHLEU.
DR   TIGRFAMs; TIGR00396; leuS_bact; 1.
DR   PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
KW   Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW   Complete proteome.
FT   SITE         41     51       "HIGH" REGION.
FT   SITE        580    584       "KMSKS" REGION.
FT   BINDING     583    583       ATP (BY SIMILARITY).
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SQ   SEQUENCE   824 AA;  95624 MW;  7CB0252A76A844EC CRC64;

  Query Match             17.2%;  Score 72.5;  DB 1;  Length 824;
  Best Local Similarity   23.3%;  Pred. No. 2.8;
  Matches   21;  Conservative   25;  Mismatches   25;  Indels   19;  Gaps    4;

Qy      4 IQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALG-APLAP-------RDAGSQRPRKKED 55
          ::|:::| ::|||: : || || |:::   : |  :| ||        | |:       |
Db    692 MELVNHLSQYLNSVPQEEWNRKLLREIVEKLTLALSPFAPHLAEEFWHDLGN-------D 744

Qy     56 NVLVE----SHEKSLGEANKADVNVLTKAK 81
          :::|:    |::    |  : :: :     |
Db    745 SLVVQQSWPSYDPKALEVEEVEIAIQINGK 774


RESULT 9
RBB1_HUMAN
ID   RBB1_HUMAN     STANDARD;      PRT;  1257 AA.
AC   P29374; Q15991; Q15992; Q15993;
DT   01-DEC-1992 (Rel. 24, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Retinoblastoma-binding protein 1 (RBBP-1).
GN   RBBP1 OR RBP1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM I).
RX   MEDLINE=94020841; PubMed=8414517;
RA   Fattaey A.R., Helin K., Dembski M.S., Dyson N., Harlow E.,
RA   Vuocolo G.A., Hanobik M.G., Haskell K.M., Oliff A., Defeo-Jones D.,
RA   Jones R.E.;
RT   "Characterization of the retinoblastoma binding proteins RBP1 and
RT   RBP2.";
RL   Oncogene 8:3149-3156(1993).
RN   [2]
RP   SEQUENCE FROM N.A., SUBCELLULAR LOCATION, AND ALTERNATIVE SPLICING.
RX   MEDLINE=93205410; PubMed=8455946;
RA   Otterson G.A., Kratzke R.A., Lin A.Y., Johnston P.G., Kaye F.J.;
RT   "Alternative splicing of the RBP1 gene clusters in an internal exon
RT   that encodes potential phosphorylation sites.";
RL   Oncogene 8:949-957(1993).
RN   [3]
RP   SEQUENCE OF 855-1203 FROM N.A. (ISOFORM I).
RX   MEDLINE=91312450; PubMed=1857421;
RA   Defeo-Jones D., Huang P.S., Jones R.E., Haskell K.M., Vuocolo G.A.,
RA   Hanobik M.G., Huber H.E., Oliff A.;
RT   "Cloning of cDNAs for cellular proteins that bind to the
RT   retinoblastoma gene product.";
RL   Nature 352:251-254(1991).
CC   -!- FUNCTION: INTERACTS WITH THE VIRAL PROTEIN-BINDING DOMAIN OF THE
CC       RETINOBLASTOMA PROTEIN.
CC   -!- SUBCELLULAR LOCATION: Nuclear.
CC   -!- ALTERNATIVE PRODUCTS: 3 isoforms; I (shown here), II and III; are
CC       produced by alternative splicing.
CC   --------------------------------------------------------------------------
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CC   --------------------------------------------------------------------------
DR   EMBL; S66427; AAB28543.1; -.
DR   EMBL; S57153; AAB25833.1; -.
DR   EMBL; S57160; AAB25834.1; -.
DR   EMBL; S57162; AAB25835.2; -.
DR   PIR; S16953; S16953.
DR   Genew; HGNC:9885; RBBP1.
DR   MIM; 180201; -.
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DR   InterPro; IPR001606; ARID.
DR   InterPro; IPR000953; Chromo.
DR   InterPro; IPR002999; Tudor.
DR   Pfam; PF01388; ARID; 1.
DR   SMART; SM00501; BRIGHT; 1.
DR   SMART; SM00298; CHROMO; 1.
DR   SMART; SM00333; TUDOR; 1.
KW   Trans-acting factor; Nuclear protein; Alternative splicing.
FT   DOMAIN      951    964       RETINOBLASTOMA PROTEIN BINDING
FT                                (POTENTIAL).
FT   VARSPLIC   1106   1174       MISSING (IN ISOFORM III).
FT   VARSPLIC   1175   1175       N -> D (IN ISOFORM III).
FT   VARSPLIC   1121   1174       MISSING (IN ISOFORM II).
FT   CONFLICT    385    385       L -> V (IN REF. 2).
FT   CONFLICT    618    618       S -> R (IN REF. 2).
FT   CONFLICT    653    653       K -> V (IN REF. 2).
FT   CONFLICT    779    779       A -> T (IN REF. 2).
FT   CONFLICT   1178   1178       D -> S (IN REF. 3).
FT   CONFLICT   1196   1201       IRKYYM -> SENIICL (IN REF. 3).
SQ   SEQUENCE   1257 AA;  142666 MW;  F5C0AB6D6ED431DC CRC64;

  Query Match             17.1%;  Score 72;  DB 1;  Length 1257;
  Best Local Similarity   26.8%;  Pred. No. 5.3;
  Matches   19;  Conservative   21;  Mismatches   27;  Indels    4;  Gaps    2;

Qy       13 HLNSMERVEWLRKKLQDVHN-FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANK 71
            ::|| ||: :|::|||::   :::| : :|  |   :| :||:  |   ||  :   :
Db     1179 NMNSTERISFLQEKLQEIRKYYMSLKSEVATIDRRRKRLKKKDREV---SHAGASMSSAS 1235

Qy       72 ADVNVLTKAKS 82
            :|  :   : |
Db     1236 SDTGMSPSSSS 1246


RESULT 10
UL25_HSV6Z
ID   UL25_HSV6Z     STANDARD;      PRT;   555 AA.
AC   P52537;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Virion protein U50.
GN   U50 OR KA11R.
OS   Human herpesvirus (type 6 / strain Z29) (HHV6).
OC   Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC   Betaherpesvirinae; Roseolovirus.
OX   NCBI_TaxID=36351;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95074921; PubMed=7983761;
RA   Stamey F.R., Dominguez G., Black J.B., Dambaugh T.R., Pellett P.E.;
RT   "Intragenomic linear amplification of human herpesvirus 6B oriLyt
RT   suggests acquisition of oriLyt by transposition.";
RL   J. Virol. 69:589-596(1995).
CC   -!- FUNCTION: VIRION PROTEIN.
CC   -!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL25,
CC       EHV-1 36, EBV BVRF1, HCMV UL77, ILTV ORF2, AND VZV 34.
CC   --------------------------------------------------------------------------
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CC   --------------------------------------------------------------------------
DR   EMBL; AF157706; AAB06348.1; -.
DR   InterPro; IPR002493; UL25.
DR   Pfam; PF01499; UL25; 1.
SQ   SEQUENCE   555 AA;  63830 MW;  68B86590DC4CD2BC CRC64;

  Query Match             16.5%;  Score 69.5;  DB 1;  Length 555;
  Best Local Similarity   35.4%;  Pred. No. 3.8;
```

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  Matches   23;  Conservative   10;  Mismatches   27;  Indels    5;  Gaps    2;

Qy       23 LRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEA----NKADVNVLT 78
            ||:|:   |    |   |       ||  :|: :||  ||  |:: :|    |  :||| |
Db       42 LREKIDQGHRDKLLRMRLKTELDALQRKMQKDSDVL-NSHLKAIEDALLFTNDGEVNVET 100

Qy       79 KAKSQ 83
            || :|
Db      101 KADTQ 105


RESULT 11
HSLU_VIBCH
ID   HSLU_VIBCH     STANDARD;      PRT;   443 AA.
AC   Q9KNQ7;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   ATP-dependent hsl protease ATP-binding subunit hslU.
GN   HSLU OR VC2674.
OS   Vibrio cholerae.
OC   Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX   NCBI_TaxID=666;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=El Tor N16961 / Serotype O1;
RX   MEDLINE=20406833; PubMed=10952301;
RA   Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA   Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA   Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA   Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA   McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA   Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA   Fraser C.M.;
RT   "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT   cholerae.";
RL   Nature 406:477-483(2000).
CC   -!- FUNCTION: CHAPERONE SUBUNIT OF A PROTEASOME-LIKE DEGRADATION
CC       COMPLEX (BY SIMILARITY).
CC   -!- SUBUNIT: INTERACTS WITH HSLV (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE CLPX CHAPERONE FAMILY. HSLU SUBFAMILY.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; AE004333; AAF95815.1; -.
DR   HSSP; P32168; 1DO2.
DR   TIGR; VC2674; -.
DR   InterPro; IPR003593; AAA_ATPase.
DR   InterPro; IPR003959; AAA_ATPase_centr.
DR   InterPro; IPR004491; Hsp_HslVU.
DR   Pfam; PF00004; AAA; 1.
DR   SMART; SM00382; AAA; 1.
DR   TIGRFAMs; TIGR00390; hslU; 1.
KW   Chaperone; ATP-binding; Complete proteome.
FT   NP_BIND      57     64       ATP (POTENTIAL).
SQ   SEQUENCE   443 AA;  49900 MW;  DAE13E82FAB6A38F CRC64;

  Query Match             15.9%;  Score 67;  DB 1;  Length 443;
  Best Local Similarity   28.8%;  Pred. No. 5.6;
  Matches   19;  Conservative   16;  Mismatches   27;  Indels    4;  Gaps    2;

Qy       13 HLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSL--GEAN 70
            |  :||:|::  ::| :     ||  |  ||||  |  :|:|::   :   | |  |: |
Db      112 HQQAMEKVKFRAEELAEERVLDALLPP--PRDAWGQAEQKEENSSTRQVFRKKLREGQLN 169

Qy       71 KADVNV 76
```

```
             :: :
Db     170 DKEIEI 175


RESULT 12
UL25_HSV6G
ID   UL25_HSV6G     STANDARD;      PRT;   378 AA.
AC   P52536;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Virion protein U50 (Fragment).
GN   U50 OR LF3.
OS   Human herpesvirus (type 6 / strain GS) (HHV6).
OC   Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC   Betaherpesvirinae; Roseolovirus.
OX   NCBI_TaxID=10369;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91374623; PubMed=1654455;
RA   Josephs S.F., Ablashi D.V., Salahuddin S.Z., Jagodzinski L.L.,
RA   Wong-Staal F., Gallo R.C.;
RT   "Identification of the human herpesvirus 6 glycoprotein H and
RT   putative large tegument protein genes.";
RL   J. Virol. 65:5597-5604(1991).
CC   -!- FUNCTION: VIRION PROTEIN.
CC   -!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL25,
CC       EHV-1 36, EBV BVRF1, HCMV UL77, ILTV ORF2, AND VZV 34.
CC   --------------------------------------------------------------------------
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CC   --------------------------------------------------------------------------
DR   EMBL; S57509; AAB19777.1; -.
DR   InterPro; IPR002493; UL25.
DR   Pfam; PF01499; UL25; 1.
FT   NON_TER     378    378
SQ   SEQUENCE   378 AA;  43459 MW;  BE8B2EF416270AB6 CRC64;

  Query Match             15.8%;  Score 66.5;  DB 1;  Length 378;
  Best Local Similarity   33.8%;  Pred. No. 5.2;
  Matches   22;  Conservative   11;  Mismatches   27;  Indels    5;  Gaps    2;

Qy      23 LRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEA----NKADVNVLT 78
           ||:|:   |    |   |       |:  :|: :||  || |:: :|    |  :||| |
Db      42 LREKIDQGHRDKLLRMRLKTELDALQKKMQKDSDVL-NSHLKAIEDALLFTNDGEVNVET 100

Qy      79 KAKSQ 83
           || :|
Db     101 KADAQ 105


RESULT 13
UL25_HSV6U
ID   UL25_HSV6U     STANDARD;      PRT;   555 AA.
AC   P52387;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Virion protein U50.
GN   U50 OR BHRF3.
OS   Human herpesvirus (type 6 / strain Uganda-1102) (HHV6).
OC   Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC   Betaherpesvirinae; Roseolovirus.
OX   NCBI_TaxID=10370;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95266321; PubMed=7747482;
RA   Gompels U.A., Nicholas J., Lawrence G., Jones M., Thomson B.J.,
RA   Martin M.E., Efstathiou S., Craxton M., Macaulay H.A.;
RT   "The DNA sequence of human herpesvirus-6: structure, coding content,
RT   and genome evolution.";
RL   Virology 209:29-51(1995).
RN   [2]
RP   SEQUENCE OF 1-378 FROM N.A.
RX   MEDLINE=93091236; PubMed=1333836;
RA   Gompels U.A., Carss A.L., Sun N., Arrand J.R.;
RT   "Infectivity determinants encoded in a conserved gene block of human
RT   herpesvirus-6.";
RL   DNA Seq. 3:25-39(1992).
CC   -!- FUNCTION: VIRION PROTEIN.
CC   -!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL25,
CC       EHV-1 36, EBV BVRF1, HCMV UL77, ILTV ORF2, AND VZV 34.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; X83413; CAA58384.1; -.
DR   EMBL; X64320; CAA45605.1; -.
DR   InterPro; IPR002493; UL25.
DR   Pfam; PF01499; UL25; 1.
SQ   SEQUENCE   555 AA;  63594 MW;  BA0C879FF56130D4 CRC64;

  Query Match             15.8%;  Score 66.5;  DB 1;  Length 555;
  Best Local Similarity   33.8%;  Pred. No. 8.2;
  Matches   22;  Conservative   11;  Mismatches   27;  Indels    5;  Gaps    2;

Qy      23 LRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEA----NKADVNVLT 78
           ||:|:   |    |   |       |:  :|: :||  || |:: :|    |  :||| |
Db      42 LREKIDQGHRDKLLRMRLKTELDALQKKMQKDSDVL-NSHLKAIEDALLFTNDGEVNVET 100

Qy      79 KAKSQ 83
           || :|
Db     101 KADAQ 105


RESULT 14
MIX1_CAEEL
ID   MIX1_CAEEL     STANDARD;      PRT;  1244 AA.
AC   Q09591;
DT   01-NOV-1997 (Rel. 35, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Mitotic chromosome and X-chromosome associated protein mix-1.
GN   MIX-1 OR M106.1.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98117254; PubMed=9458050;
RA   Lieb J.D., Albrecht M.R., Chuang P.T., Meyer B.J.;
RT   "MIX-1: an essential component of the C. elegans mitotic machinery
RT   executes X chromosome dosage compensation.";
RL   Cell 92:265-277(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RA   Palmer S.;
RL   Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Required for X-chromosome dosage compensation. Member of
CC       the dosage compensation complex that associates specifically with
CC       hermaphrodite X chromosomes to reduce their gene expression during
CC       interphase.
CC   -!- SUBCELLULAR LOCATION: Nuclear.
CC   -!- DOMAIN: CONSISTS OF TWO PUTATIVE CENTRAL COILED-COIL REGIONS
```

```
CC       FLANKED BY PUTATIVE GLOBULAR REGIONS AT THE N- AND C-TERMINUS.
CC   -!- SIMILARITY: BELONGS TO THE SMC FAMILY.
CC   --------------------------------------------------------------------------
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CC   --------------------------------------------------------------------------
DR   EMBL; U96387; AAC47834.1; -.
DR   EMBL; Z46935; CAA87054.1; -.
DR   EMBL; AL031266; CAA20330.1; -.
DR   EMBL; Z46794; CAA20330.1; JOINED.
DR   EMBL; Z46935; CAA20330.1; JOINED.
DR   EMBL; Z46794; CAA86786.1; -.
DR   EMBL; AL031266; CAA86786.1; JOINED.
DR   EMBL; Z46935; CAA86786.1; JOINED.
DR   WormPep; M106.1; CE18083.
DR   InterPro; IPR003405; SMC_C.
DR   InterPro; IPR003395; SMC_N.
DR   Pfam; PF02463; SMC_N; 1.
DR   Pfam; PF02483; SMC_C; 1.
DR   ProDom; PD000006; ABC_transportr; 1.
KW   ATP-binding; Coiled coil; Nuclear protein.
FT   NP_BIND      32     39       ATP (POTENTIAL).
FT   DOMAIN      245    350       COILED COIL (POTENTIAL).
FT   DOMAIN      415    479       COILED COIL (POTENTIAL).
FT   DOMAIN      702   1043       COILED COIL (POTENTIAL).
FT   DOMAIN     1109   1135       ALA/ASP-RICH (DA-BOX).
FT   DOMAIN     1239   1242       POLY-ASP.
SQ   SEQUENCE   1244 AA;  140341 MW;  255FD9C3D8C4AA49 CRC64;

  Query Match             15.4%;  Score 65;  DB 1;  Length 1244;
  Best Local Similarity   26.8%;  Pred. No. 31;
  Matches   22;  Conservative   16;  Mismatches   34;  Indels   10;  Gaps    2;

Qy          6 LMHNLGKHLNSMER----VEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVES 61
              :: :|  |    |:    :|   | |:|| : :     :  :|  ||  ||||   |::
Db        756 VVRDLKVHSEEYEKNQAEIEATVKTLKDVEDKIKTLESMKNKDKNSQEKRKKELTALLQK 815

Qy         62 HE------KSLGEANKADVNVL 77
               |      |: ||  : :| :|
Db        816 AEQTVAQNKNRGEKARREVMLL 837


RESULT 15
KGUA_CHLPN
ID   KGUA_CHLPN     STANDARD;      PRT;   205 AA.
AC   Q9Z961;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Guanylate kinase (EC 2.7.4.8) (GMP kinase).
GN   GMK OR CPN0120 OR CP0653.
OS   Chlamydia pneumoniae (Chlamydophila pneumoniae).
OC   Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
OX   NCBI_TaxID=83558;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CWL029;
RX   MEDLINE=99206606; PubMed=10192388;
RA   Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
RA   Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RT   "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
RL   Nat. Genet. 21:385-389(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=AR39;
RX   MEDLINE=20150255; PubMed=10684935;
RA   Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA   White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
RA   Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA   Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA   Eisen J., Fraser C.M.;
RT   "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RT   pneumoniae AR39.";
RL   Nucleic Acids Res. 28:1397-1406(2000).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=J138;
RX   MEDLINE=20330349; PubMed=10871362;
RA   Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA   Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT   "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RT   from Japan and CWL029 from USA.";
RL   Nucleic Acids Res. 28:2311-2314(2000).
CC   -!- FUNCTION: ESSENTIAL FOR RECYCLING GMP AND INDIRECTLY, CGMP.
CC   -!- CATALYTIC ACTIVITY: ATP + GMP = ADP + GDP.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE GUANYLATE KINASE FAMILY.
CC   --------------------------------------------------------------------------
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CC   --------------------------------------------------------------------------
DR   EMBL; AE001598; AAD18273.1; -.
DR   EMBL; AE002223; AAF38468.1; -.
DR   EMBL; AP002545; BAA98331.1; -.
DR   HSSP; P15454; 1GKY.
DR   PHCI-2DPAGE; Q9Z961; -.
DR   TIGR; CP0653; -.
DR   InterPro; IPR000619; Guanylate_kin.
DR   Pfam; PF00625; Guanylate_kin; 1.
DR   SMART; SM00072; GuKc; 1.
DR   PROSITE; PS00856; GUANYLATE_KINASE_1; 1.
DR   PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
KW   Transferase; Kinase; ATP-binding; Complete proteome.
FT   NP_BIND      26     33       ATP (BY SIMILARITY).
SQ   SEQUENCE   205 AA;  23367 MW;  84A5422A624555F5 CRC64;

  Query Match             15.3%;  Score 64.5;  DB 1;  Length 205;
  Best Local Similarity   26.1%;  Pred. No. 4.3;
  Matches   24;  Conservative   21;  Mismatches   30;  Indels   17;  Gaps    4;

Qy          3 EIQLMHNLGKHLNSMERVE---WLRKKLQDVHNFVA------LGAPLAPR--DAGSQRPR 51
              ||: : :||||  ::  ::   ::| ::  |  |:|      |   || |  : ||||
Db        102 EIERIWSLGKHAVAVIDIQGALFIRSRMPSVSIFIAPPSQEELERRLASRGSEEGSQRKE 161

Qy         52 KKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 83
              : | :::       |  ||: |  ::    :|
Db        162 RLEHSLI------ELAAANQFDYVIINDDLNQ 187


Search completed: March 13, 2003, 15:00:50
Job time : 12.291 secs
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                    GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on:         March 13, 2003, 14:57:54 ; Search time 32.209 Seconds
                                           (without alignments)
                                           530.968 Million cell updates/sec

Title:          US-09-636-530-2
Perfect score:  422
Sequence:       1 VSEIQLMHNLGKHLNSMERV..........KSLGEANKADVNVLTKAKSQ 83

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters:      671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       SPTREMBL_21:*
                1:  sp_archea:*
                2:  sp_bacteria:*
                3:  sp_fungi:*
                4:  sp_human:*
                5:  sp_invertebrate:*
                6:  sp_mammal:*
                7:  sp_mhc:*
                8:  sp_organelle:*
                9:  sp_phage:*
                10:  sp_plant:*
                11:  sp_rodent:*
                12:  sp_virus:*
                13:  sp_vertebrate:*
                14:  sp_unclassified:*
                15:  sp_rvirus:*
                16:  sp_bacteriap:*
                17:  sp_archeap:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
               %
Result       Query
  No.  Score Match Length DB  ID                        Description
 -------------------------------------------------------------------------------
   1    368   87.2     86  6  Q9N1V0                  Q9n1v0 equus cabal
   2    358   84.8    115  6  Q9GL67                  Q9gl67 felis silve
   3    307   72.7    115 11   Q9Z0L6                  Q9z0l6 mus musculu
   4     84   19.9     31 11   Q91Y91                  Q91y91 peromyscus
   5     84   19.9     31 11   Q91Y90                  Q91y90 peromyscus
   6   79.5   18.8    163 13   Q9I8E9                  Q9i8e9 fugu rubrip
   7   78.5   18.6    162 13   Q9I8U2                  Q9i8u2 sparus aura
   8     73   17.3    565 16   Q99WC5                  Q99wc5 staphylococ
   9     69   16.4    334 17   Q8TJX5                  Q8tjx5 methanosarc
  10   68.5   16.2    256  5  Q9VDC2                  Q9vdc2 drosophila
  11     68   16.1    607 16   Q8RG65                  Q8rg65 fusobacteri
  12   67.5   16.0   1156 16   O66878                  O66878 aquifex aeo
  13     67   15.9    674 10   O23544                  O23544 arabidopsis
  14     66   15.6    215  5  O17915                  O17915 caenorhabdi
  15     66   15.6    341 17   Q97CE4                  Q97ce4 thermoplasm
  16     66   15.6    396 16   Q97MB3                  Q97mb3 clostridium
  17     66   15.6    886 10  Q8W3D7                   Q8w3d7 oryza sativ
  18     66   15.6    896 10  Q9SHT1                   Q9sht1 arabidopsis
  19     66   15.6   1175 10  Q8S8B4                   Q8s8b4 arabidopsis
  20   65.5   15.5    861 10  Q9AVZ9                   Q9avz9 guillardia
  21     65   15.4    189 11   Q922S6                  Q922s6 mus musculu
  22     65   15.4    283  9  Q9AZW5                  Q9azw5 bacteriopha
  23     65   15.4    283 16   Q9CFN5                   Q9cfn5 lactococcus
  24     65   15.4    323 11   Q9CWX9                  Q9cwx9 mus musculu
  25     65   15.4    377  5  Q9XY80                  Q9xy80 speleonecte
  26     65   15.4    873  4  Q9NYU3                  Q9nyu3 homo sapien
  27     65   15.4   1226  4  Q9NZB6                  Q9nzb6 homo sapien
  28     65   15.4   1228 11   Q9JKB5                   Q9jkb5 rattus norv
  29   64.5   15.3    264 13  Q9PS76                   Q9ps76 gallus gall
  30   64.5   15.3    292 13  Q9PS77                   Q9ps77 gallus gall
  31   64.5   15.3    321  5  Q94940                  Q94940 drosophila
  32   64.5   15.3    495  4  Q9NUP4                  Q9nup4 homo sapien
  33   64.5   15.3    668  6  Q9GLG4                  Q9glg4 sus scrofa
  34   64.5   15.3    792 13   O13110                   O13110 gallus gall
  35   64.5   15.3   1018  3  Q9UST0                  Q9ust0 schizosacch
  36   64.5   15.3   1118 13   Q98951                   Q98951 gallus gall
  37   64.5   15.3   1137 13   O93569                   O93569 gallus gall
  38   64.5   15.3   1137 13   O12942                   O12942 gallus gall
  39     64   15.2    166  4  Q9UF62                  Q9uf62 homo sapien
  40     64   15.2    369  2  Q9F537                  Q9f537 escherichia
  41     64   15.2    459  4  Q9H915                  Q9h915 homo sapien
  42     64   15.2    667 17   Q8TLG5                   Q8tlg5 methanosarc
  43     64   15.2    784  4  Q9H5A0                  Q9h5a0 homo sapien
  44     64   15.2   1004 16   Q8XL47                   Q8xl47 clostridium
  45   63.5   15.0    376 11   Q99KR6                   Q99kr6 mus musculu


                              ALIGNMENTS


RESULT 1
Q9N1V0
ID   Q9N1V0      PRELIMINARY;      PRT;    86 AA.
AC   Q9N1V0;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Parathyroid hormone (Fragment).
GN   PTH.
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20082971; PubMed=10613847;
RA   Caetano A.R., Shiue Y.L., Lyons L.A., O'Brien S.J., Laughlin T.F.,
RA   Bowling A.T., Murray J.D.;
RT   "A comparative gene map of the horse (Equus caballus).";
RL   Genome Res. 9:1239-1249(1999).
DR   EMBL; AF134233; AAF62347.1; -.
DR   HSSP; P01270; 1HPY.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   Pfam; PF01279; Parathyroid; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   SMART; SM00087; PTH; 1.
DR   PROSITE; PS00335; PARATHYROID; 1.
FT   NON_TER      1      1
SQ   SEQUENCE   86 AA;  9805 MW;  253184EA681A2022 CRC64;

  Query Match             87.2%;  Score 368;  DB 6;  Length 86;
  Best Local Similarity   84.3%;  Pred. No. 1.8e-33;
  Matches   70;  Conservative    8;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
             ||||||||||||||||:||||||||||||||||:|||||:  || |||||||||||||:|
Db       4 VSEIQLMHNLGKHLNSVERVEWLRKKLQDVHNFIALGAPIFHRDGGSQRPRKKEDNVLIE 63
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Qy         61 SHEKSLGEANKADVNVLTKAKSQ 83
              ||: |||||:||||:||:| |||
Db         64 SHQXSLGEADKADVDVLSKTKSQ 86


RESULT 2
Q9GL67
ID   Q9GL67      PRELIMINARY;      PRT;   115 AA.
AC   Q9GL67;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Preproparathyroid hormone precursor.
GN   PTH.
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Toribio R.E., Kohn C.W., Leone G.W., Capen C.C., Rosol T.J.;
RT   "Molecular cloning of feline preproparathyroid hormone.";
RL   Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF309967; AAG30545.1; -.
DR   HSSP; P01268; 1ZWC.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   Pfam; PF01279; Parathyroid; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   SMART; SM00087; PTH; 1.
DR   PROSITE; PS00335; PARATHYROID; 1.
KW   Signal.
FT   SIGNAL        1     25       POTENTIAL.
FT   CHAIN        32    115       PARATHYROID HORMONE.
SQ   SEQUENCE   115 AA;  12921 MW;  80CD557CC6A1A47E CRC64;

  Query Match             84.8%;  Score 358;  DB 6;  Length 115;
  Best Local Similarity   83.1%;  Pred. No. 3.3e-32;
  Matches   69;  Conservative    8;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
              ||||| ||||||||:|:|||||||:||||||||||||||:| || ||||||||||||  |
Db         33 VSEIQFMHNLGKHLSSVERVEWLRRKLQDVHNFVALGAPIAHRDGGSQRPRKKEDNVPAE 92

Qy         61 SHEKSLGEANKADVNVLTKAKSQ 83
              :|:||||||:||||:|| |||||
Db         93 NHQKSLGEADKADVDVLIKAKSQ 115


RESULT 3
Q9Z0L6
ID   Q9Z0L6      PRELIMINARY;      PRT;   115 AA.
AC   Q9Z0L6;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Parathyroid hormone precursor.
GN   PTH.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SV;
RA   Karaplis A.C., He B., Hiou-Tim F.F.T., Al-Akad B., Kronenberg H.M.;
RT   "Cloning of the murine gene encoding parathyroid hormone: genomic
RT   organization and nucleotide sequence.";
RL   Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF066075; AAC99656.1; -.
DR   HSSP; P01270; 1ZWB.
DR   MGD; MGI:97799; Pth.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   Pfam; PF01279; Parathyroid; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   SMART; SM00087; PTH; 1.
DR   PROSITE; PS00335; PARATHYROID; 1.
KW   Signal.
FT   SIGNAL        1     25       POTENTIAL.
FT   CHAIN        32    115       PARATHYROID HORMONE.
SQ   SEQUENCE   115 AA;  12825 MW;  DA43FABBCB4E2FD9 CRC64;

  Query Match             72.7%;  Score 307;  DB 11;  Length 115;
  Best Local Similarity   69.9%;  Pred. No. 1.5e-26;
  Matches   58;  Conservative   13;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
              |||||||||||||| ||||::|||:||||:||||:||  :| ||   |:| |||:||||:
Db         33 VSEIQLMHNLGKHLASMERMQWLRRKLQDMHNFVSLGVQMAARDGSHQKPTKKEENVLVD 92

Qy         61 SHEKSLGEANKADVNVLTKAKSQ 83
               : ||||| :||||:|| |:|||
Db         93 GNPKSLGEGDKADVDVLVKSKSQ 115


RESULT 4
Q91Y91
ID   Q91Y91      PRELIMINARY;      PRT;    31 AA.
AC   Q91Y91;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Parathyroid hormone (Fragment).
GN   PTH.
OS   Peromyscus polionotus (Oldfield mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC   Peromyscus.
OX   NCBI_TaxID=42413;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Prince K.L., Dewey M.J.;
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF382952; AAK63071.1; -.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   Pfam; PF01279; Parathyroid; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   PROSITE; PS00335; PARATHYROID; UNKNOWN_1.
FT   NON_TER       1      1
FT   NON_TER      31     31
SQ   SEQUENCE    31 AA;  3461 MW;  A208B0E772B9B55B CRC64;

  Query Match             19.9%;  Score 84;  DB 11;  Length 31;
  Best Local Similarity   94.4%;  Pred. No. 0.02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VSEIQLMHNLGKHLNSME 18
              |||||||||||||| |||
Db         14 VSEIQLMHNLGKHLASME 31


RESULT 5
Q91Y90
ID   Q91Y90      PRELIMINARY;      PRT;    31 AA.
AC   Q91Y90;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Parathyroid hormone (Fragment).
GN   PTH.
OS   Peromyscus maniculatus (Deer mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC   Peromyscus.
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OX   NCBI_TaxID=10042;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Prince K.L., Dewey M.J.;
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF382953; AAK63072.1; -.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   Pfam; PF01279; Parathyroid; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   PROSITE; PS00335; PARATHYROID; UNKNOWN_1.
FT   NON_TER       1      1
FT   NON_TER      31     31
SQ   SEQUENCE   31 AA;  3461 MW;  A208B0E772B9B55B CRC64;

  Query Match             19.9%;  Score 84;  DB 11;  Length 31;
  Best Local Similarity   94.4%;  Pred. No. 0.02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         1 VSEIQLMHNLGKHLNSME 18
             |||||||||||||| |||
Db        14 VSEIQLMHNLGKHLASME 31


RESULT 6
Q9I8E9
ID   Q9I8E9      PRELIMINARY;      PRT;   163 AA.
AC   Q9I8E9;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Parathyroid hormone-related protein precursor.
GN   PTHRP.
OS   Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetraodontidae; Takifugu.
OX   NCBI_TaxID=31033;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20314478; PubMed=10854780;
RA   Power D.M., Flannigan J., Ingleton P.M., Canario A.V.M., Danks J.,
RA   Elgar G., Clark M.S.;
RT   "Genomic structure and expression of parathyroid hormone-related
RT   protein in a teleost, Fugu rubripes.";
RL   Gene 250:67-79(2000).
DR   EMBL; AJ249391; CAB94712.1; -.
DR   HSSP; P12272; 1BZG.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003626; PTH_related.
DR   Pfam; PF01279; Parathyroid; 1.
DR   ProDom; PD013225; PTH_related; 1.
DR   SMART; SM00087; PTH; 1.
KW   Signal.
FT   SIGNAL        1     34       POTENTIAL.
SQ   SEQUENCE   163 AA;  18698 MW;  3AC5F2C764732278 CRC64;

  Query Match             18.8%;  Score 79.5;  DB 13;  Length 163;
  Best Local Similarity   27.5%;  Pred. No. 0.44;
  Matches   30;  Conservative   10;  Mismatches   36;  Indels   33;  Gaps    4;

Qy         1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
             ||  ||||: |: |    |  || | |::||       |:  |     : :    | |
Db        39 VSHAQLMHDKGRSLQEFRRRMWLHKLLEEVHTANEEAPPVQSR----TQTQTFSGNSL-- 92

Qy        61 SHEKSLG--------------------EANKA------DVNVLTKAKSQ 83
              |||  |                    | |||       : : || | :
Db        93 -HEKPPGATKNLPDRFSLDREGTNLPQETNKALAYKDQPLKLATKRKKK 140


RESULT 7
Q9I8U2
ID   Q9I8U2      PRELIMINARY;      PRT;   162 AA.
AC   Q9I8U2;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Parathyroid hormone-related protein.
GN   PTHRP.
OS   Sparus aurata (Gilthead sea bream).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;
OC   Sparidae; Sparus.
OX   NCBI_TaxID=8175;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=KIDNEY;
RX   MEDLINE=20304721; PubMed=10843788;
RA   Flanagan J.A., Power D.M., Bendell L.A., Guerreiro P.M., Fuentes J.,
RA   Clark M.S., Canario A.V., Danks J.A., Brown B.L., Ingleton P.M.;
RT   "Cloning of the cDNA for sea bream (Sparus aurata) parathyroid
RT   hormone-related protein.";
RL   Gen. Comp. Endocrinol. 118:373-382(2000).
DR   EMBL; AF197904; AAF79073.1; -.
DR   HSSP; P12272; 1BZG.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003626; PTH_related.
DR   Pfam; PF01279; Parathyroid; 1.
DR   ProDom; PD013225; PTH_related; 1.
DR   SMART; SM00087; PTH; 1.
SQ   SEQUENCE   162 AA;  18722 MW;  6E8D5E07F9E5EDC9 CRC64;

  Query Match             18.6%;  Score 78.5;  DB 13;  Length 162;
  Best Local Similarity   28.4%;  Pred. No. 0.57;
  Matches   31;  Conservative   11;  Mismatches   32;  Indels   35;  Gaps    5;

Qy         1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
             ||  ||||: |: |   :|  || : |::||   |   |:  |     : :    | |
Db        39 VSHAQLMHDKGRSLQEFKRRMWLHELLEEVH--TADDRPVQSR----TQSQTFSGNAL-- 90

Qy        61 SHEKSLG--------------------EANKA------DVNVLTKAKSQ 83
              |||  |                    | |||       : | || | :
Db        91 -HEKPPGATKNIPDRFRLDREGPNLPQETNKALAYKDQPLKVATKRKKK 138


RESULT 8
Q99WC5
ID   Q99WC5      PRELIMINARY;      PRT;   565 AA.
AC   Q99WC5;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   DNA polymerase III gamma and tau subunits.
GN   DNAX OR SAV0478 OR SA0436.
OS   Staphylococcus aureus (strain Mu50 / ATCC 700699), and
OS   Staphylococcus aureus (strain N315).
OC   Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC   Staphylococcus.
OX   NCBI_TaxID=158878, 158879;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   SPECIES=S.aureus (strain Mu50), and S.aureus (strain N315);
RX   MEDLINE=21311952; PubMed=11418146;
RA   Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA   Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA   Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA   Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA   Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA   Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA   Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT   "Whole genome sequencing of meticillin-resistant Staphylococcus
RT   aureus.";
RL   Lancet 357:1225-1240(2001).
DR   EMBL; AP003359; BAB56640.1; -.
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DR   EMBL; AP003130; BAB41666.1; -.
DR   InterPro; IPR003593; AAA_ATPase.
DR   InterPro; IPR003959; AAA_ATPase_centr.
DR   InterPro; IPR001270; Chaprnin_clpA/B.
DR   InterPro; IPR000345; CytC_heme_bind.
DR   InterPro; IPR000463; Fatty_acid_BP.
DR   InterPro; IPR000862; RFCdomain.
DR   Pfam; PF00004; AAA; 1.
DR   PRINTS; PR00300; CLPPROTEASEA.
DR   SMART; SM00382; AAA; 1.
DR   PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR   PROSITE; PS00214; FABP; UNKNOWN_1.
KW   Complete proteome.
SQ   SEQUENCE   565 AA;  63471 MW;  F29A7F07095F02AA CRC64;

  Query Match             17.3%;  Score 73;  DB 16;  Length 565;
  Best Local Similarity   29.4%;  Pred. No. 10;
  Matches   20;  Conservative   15;  Mismatches   23;  Indels   10;  Gaps    2;

Qy     14 LNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRP----RKKEDNVLVESHEKSLGEA 69
          |  ||::|      |::    | |  :||    |::|    :| ::   ::   | | :|
Db    376 LQRMEQLE------QELKTLKAQGVSVAPAQKSSKKPARGIQKSKNAFSMQQIAKVLDKA 429

Qy     70 NKADVNVL 77
          ||||: :|
Db    430 NKADIKLL 437


RESULT 9
Q8TJX5
ID   Q8TJX5      PRELIMINARY;      PRT;   334 AA.
AC   Q8TJX5;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Amidinotransferase.
GN   MA3652.
OS   Methanosarcina acetivorans.
OC   Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
OC   Methanosarcinaceae; Methanosarcina.
OX   NCBI_TaxID=2214;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C2A / ATCC 35395 / DSM 2834;
RX   MEDLINE=21929760; PubMed=11932238;
RA   Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA   FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
RA   Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,
RA   Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA   Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
RA   Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,
RA   Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA   Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
RA   Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
RA   Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA   Metcalf W.W., Birren B.;
RT   "The genome of Methanosarcina acetivorans reveals extensive metabolic
RT   and physiological diversity.";
RL   Genome Res. 12:532-542(2002).
DR   EMBL; AE011074; AAM07007.1; -.
KW   Transferase; Complete proteome.
SQ   SEQUENCE   334 AA;  37958 MW;  0465FE751248EA83 CRC64;

  Query Match             16.4%;  Score 69;  DB 17;  Length 334;
  Best Local Similarity   40.4%;  Pred. No. 15;
  Matches   19;  Conservative    6;  Mismatches   18;  Indels    4;  Gaps    2;

Qy      3 EIQLMHNLGKHLNSMERVEWLRKKLQD---VHNFVALGAPLAPRDAG 46
          :: : |: |    ||: :||||  | |   ||  |||||     | |
Db    189 DVLVGHSQGNFATSMKGIEWLRNYLGDEYTVHT-VALGADYLHLDDG 234


RESULT 10
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Q9VDC2
ID   Q9VDC2      PRELIMINARY;      PRT;   256 AA.
AC   Q9VDC2;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   CG5919 protein.
GN   CG5919.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BERKELEY;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
DR   EMBL; AE003734; AAF55875.1; -.
DR   FlyBase; FBgn0038876; CG5919.
DR   InterPro; IPR002667; IPP_isomerase.
DR   InterPro; IPR000086; NUDIX_hydrolase.
DR   Pfam; PF00293; NUDIX; 1.
DR   ProDom; PD004109; IPP_isomerase; 1.
SQ   SEQUENCE   256 AA;  29769 MW;  82764D6327E7B377 CRC64;

  Query Match             16.2%;  Score 68.5;  DB 5;  Length 256;
  Best Local Similarity   31.1%;  Pred. No. 13;
  Matches   23;  Conservative   12;  Mismatches   22;  Indels   17;  Gaps    3;

Qy     10 LGKHLN-SMERVEWLR---------KKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLV 59
          |   ||  : || |||         |  : |    |:  ||       |    ||  :||
Db      2 LASRLNLLLPRVSWLRGCSTTAVGQKHQRQVPTEFAVHDPL-------QAHALKEQCILV 54

Qy     60 ESHEKSLGEANKAD 73
          :::::::| |:|||
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Db         55 DANDQAIGAASKAD 68


RESULT 11
Q8RG65
ID   Q8RG65      PRELIMINARY;      PRT;   607 AA.
AC   Q8RG65;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Glucosamine--fructose-6-phosphate aminotransferase (EC 2.6.1.16).
GN   FN0452.
OS   Fusobacterium nucleatum (subsp. nucleatum).
OC   Bacteria; Fusobacteria; Fusobacterium.
OX   NCBI_TaxID=76856;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 25586;
RX   MEDLINE=21886394; PubMed=11889109;
RA   Kapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
RA   Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
RA   Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A.,
RA   Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
RA   Fonstein M., Kyrpides N., Overbeek R.;
RT   "Genome sequence and analysis of the oral bacterium Fusobacterium
RT   nucleatum strain ATCC 25586.";
RL   J. Bacteriol. 184:2005-2018(2002).
DR   EMBL; AE010557; AAL94648.1; -.
KW   Transferase; Aminotransferase; Complete proteome.
SQ   SEQUENCE   607 AA;  67899 MW;  9E08127E00EEE35A CRC64;

  Query Match             16.1%;  Score 68;  DB 16;  Length 607;
  Best Local Similarity   25.6%;  Pred. No. 40;
  Matches   21;  Conservative   21;  Mismatches   34;  Indels    6;  Gaps    3;

Qy      1 VSEIQLM-HNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLV 59
          :|:| |:  |: | ::  |::  : ||::|: |   ||  :  : |    : || | :
Db    434 ISDISLLKENVVKLISEKEKIHDIAKKIKDIKNGFYLGRGIDEKVAREGSLKMKEINYI- 492

Qy     60 ESHEKSL--GEANKADVNVLTK 79
            | ::|  ||     : :: |
Db    493 --HTEALPAGELKHGSIALIEK 512


RESULT 12
O66878
ID   O66878      PRELIMINARY;      PRT;  1156 AA.
AC   O66878;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Chromosome assembly protein homolog.
GN   XCPC OR AQ_629.
OS   Aquifex aeolicus.
OC   Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
OX   NCBI_TaxID=63363;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=VF5;
RX   MEDLINE=98196666; PubMed=9537320;
RA   Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA   Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R.,
RA   Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT   "The complete genome of the hyperthermophilic bacterium Aquifex
RT   aeolicus.";
RL   Nature 392:353-358(1998).
DR   EMBL; AE000699; AAC06839.1; -.
DR   InterPro; IPR003439; ABC_transportr.
DR   InterPro; IPR005289; GTP-bindding_dom.
DR   InterPro; IPR003405; SMC_C.
DR   InterPro; IPR003395; SMC_N.
DR   InterPro; IPR002017; Spectrin.
DR   Pfam; PF02483; SMC_C; 1.
DR   Pfam; PF02463; SMC_N; 1.
DR   TIGRFAMs; TIGR00650; MG442; 1.
DR   PROSITE; PS00211; ABC_TRANSPORTER; UNKNOWN_1.
KW   Complete proteome.
SQ   SEQUENCE   1156 AA;  135563 MW;  B12DB30F70C0CE49 CRC64;

  Query Match             16.0%;  Score 67.5;  DB 16;  Length 1156;
  Best Local Similarity   29.0%;  Pred. No. 96;
  Matches   27;  Conservative   16;  Mismatches   25;  Indels   25;  Gaps    4;

Qy      1 VSEIQLMHNLGKHLNSMER--------VEWLRKKLQDVHNFVALGAPLAPRDAGSQRPR- 51
          ||||:      | ||  :||        :|:| |::|:             |:  ::| :
Db    794 VSEIE------KSLNEIERELNKKTYELEYLEKEIQEKER---------EREYLTERIKS 838

Qy     52 -KKEDNVLVESHEKSLGEANKADVNVLTKAKSQ 83
           |||   |:   ||:| |  :|:| |    | :
Db    839 LKKEIENLILFKEKTLQEVKEAEVKVYDYIKQK 871


RESULT 13
O23544
ID   O23544      PRELIMINARY;      PRT;   674 AA.
AC   O23544; O23543;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Hypothetical 75.3 kDa protein.
GN   AT4G17000.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Bevan M., Stiekema W., Murphy G., Wambutt R., Pohl T., Terryn N.,
RA   Kreis M., Kavanagh T., Entian K.D., Rieger M., James R.,
RA   Puigdomenech P., Hatzopoulos P., Obermaier B., Duesterhoft A.,
RA   Jones J., Palme K., Ansorge W., Delseny M., Bancroft I., Mewes H.W.,
RA   Schueller C., Chalwatzis N.;
RL   Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   EU Arabidopsis sequencing project;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; Z97342; CAB10480.1; -.
DR   EMBL; AL161545; CAB80971.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   674 AA;  75341 MW;  F846AD8C3AC63C34 CRC64;

  Query Match             15.9%;  Score 67;  DB 10;  Length 674;
  Best Local Similarity   24.3%;  Pred. No. 58;
  Matches   18;  Conservative   21;  Mismatches   31;  Indels    4;  Gaps    2;

Qy     12 KHLNSMER-VEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKK---EDNVLVESHEKSLG 67
          | ::  ::  |  |:|:::   : |    || ||  :       |   ::  :|||:  :  |
Db    271 KQIDQKDKGVSTLKKRVKKKEDPVPSSDPLKPYDSNGMEVEDKTSRDEELLVENKSEELS 330

Qy     68 EANKADVNVLTKAK 81
          : :||::|   :|:
Db    331 DTSKANMNNQLQAR 344


RESULT 14
O17915
ID   O17915      PRELIMINARY;      PRT;   215 AA.
AC   O17915;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   K01G5.4 protein.
GN   K01G5.4.
OS   Caenorhabditis elegans.
```

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OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Wall M.;
RL   Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99069613; PubMed=9851916;
RA   none;
RT   "Genome sequence of the nematode C.elegans: A platform for
RT   investigating biology.";
RL   Science 282:2012-2018(1998).
CC   -!- FUNCTION: GTP-BINDING PROTEIN INVOLVED IN NUCLEOCYTOPLASMIC
CC       TRANSPORT. REQUIRED FOR THE IMPORT OF PROTEIN INTO THE NUCLEUS AND
CC       ALSO FOR RNA EXPORT (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE RAN FAMILY IN THE RAS SUPERFAMILY.
DR   EMBL; Z92803; CAB07240.1; -.
DR   HSSP; P17080; 1RRP.
DR   InterPro; IPR002041; RAN.
DR   InterPro; IPR001806; Ras_trnsfrmng.
DR   InterPro; IPR005225; Small_GTP.
DR   InterPro; IPR003575; Small_GTPase.
DR   Pfam; PF00071; ras; 1.
DR   PRINTS; PR00627; GTPRANTC4.
DR   PRINTS; PR00449; RASTRNSFRMNG.
DR   SMART; SM00176; RAN; 1.
DR   SMART; SM00010; small_GTPase; 1.
DR   TIGRFAMs; TIGR00231; small_GTP; 1.
DR   PROSITE; PS01115; RAN; 1.
KW   GTP-binding; Nuclear protein; Protein transport.
SQ   SEQUENCE   215 AA;  24254 MW;  90B32613588745E5 CRC64;

  Query Match             15.6%;  Score 66;  DB 5;  Length 215;
  Best Local Similarity   38.2%;  Pred. No. 20;
  Matches   21;  Conservative    7;  Mismatches   17;  Indels   10;  Gaps    3;

Qy       22 WLRKKLQDVHN--FVALGAPLAPRDAGSQRPRKKEDNVLVESHEKSLGEANKADV 74
            || :||    |  |||: | |||       |  : |  ::  :|| |  | |||:
Db      162 WLARKLLGDPNLEFVAMPA-LAP-------PEVQMDPAMIAEYEKDLDNAAKADL 208


RESULT 15
Q97CE4
ID   Q97CE4      PRELIMINARY;      PRT;   341 AA.
AC   Q97CE4;
DT   01-OCT-2001 (TrEMBLrel. 18, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Hypothetical protein TV0158.
GN   TV0158 OR TVG0169833.
OS   Thermoplasma volcanium.
OC   Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
OC   Thermoplasmataceae; Thermoplasma.
OX   NCBI_TaxID=50339;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=GSS1 / DSM 4299 / JCM 9571;
RX   MEDLINE=20570466; PubMed=11121031;
RA   Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S.,
RA   Kawashima-Ohya Y., Watanabe K., Yamazaki M., Kanehori K., Kawamoto T.,
RA   Nunoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;
RT   "Archaeal adaptation to higher temperatures revealed by genomic
RT   sequence of Thermoplasma volcanium.";
RL   Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).
DR   EMBL; AP000991; BAB59300.1; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   341 AA;  38858 MW;  D180D7AA274D6C69 CRC64;

  Query Match             15.6%;  Score 66;  DB 17;  Length 341;
  Best Local Similarity   27.2%;  Pred. No. 34;
  Matches   22;  Conservative   16;  Mismatches   25;  Indels   18;  Gaps    5;

Qy        1 VSEIQLMHNLGKHLNSMERVEWLRKKLQD--VHNFVALGAPLAPRDAGSQRPRKKEDNVL 58
            :  ::  ||||  ||::| |: ||  :|:     |  |            |||  ||:::
Db       19 IDSVEETHNLG--LNALE-VQLLRVNVQENSAEEFAGL------------RPRDVEDSII 63

Qy       59 VESHEKSLGEANKADVNVLTK 79
            ::   :   | |   | : |:
Db       64 IDVMRQD-EEGNYVSVGINTE 83

Search completed: March 13, 2003, 15:01:50
Job time : 35.209 secs
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                         GenCore version 5.1.4_p5_4578
                 Copyright (c) 1993 - 2003  Compugen Ltd.

OM protein - protein search, using sw model

Run on:         March 13, 2003, 14:48:44 ; Search time 176.53 Seconds
                                           (without alignments)
                                           303.138 Million cell updates/sec

Title:          US-09-636-530-2
Perfect score:  422
Sequence:       1 VSEIQLMHNLGKHLNSMERV..........KSLGEANKADVNVLTKAKSQ 83

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters:      4569144

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Pending_Patents_AA_Main:*
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                2:  /cgn2_6/ptodata/2/paa/US06_COMB.pep:*
                3:  /cgn2_6/ptodata/2/paa/US07_COMB.pep:*
                4:  /cgn2_6/ptodata/2/paa/US080_COMB.pep:*
                5:  /cgn2_6/ptodata/2/paa/US081_COMB.pep:*
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                7:  /cgn2_6/ptodata/2/paa/US083_COMB.pep:*
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                10:  /cgn2_6/ptodata/2/paa/US086_COMB.pep:*
                11:  /cgn2_6/ptodata/2/paa/US087_COMB.pep:*
                12:  /cgn2_6/ptodata/2/paa/US088_COMB.pep:*
                13:  /cgn2_6/ptodata/2/paa/US089_COMB.pep:*
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                15:  /cgn2_6/ptodata/2/paa/US091_COMB.pep:*
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                21:  /cgn2_6/ptodata/2/paa/US097_COMB.pep:*
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                23:  /cgn2_6/ptodata/2/paa/US099_COMB.pep:*
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                27:  /cgn2_6/ptodata/2/paa/US60_COMB.pep:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                  SUMMARIES
                       %
Result              Query
   No.    Score    Match Length DB  ID                     Description
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     1      422    100.0     83  20  US-09-636-530-2         Sequence 2, Appli
     2      422    100.0     83  23  US-09-928-047B-1        Sequence 1, Appli
     3      422    100.0     83  23  US-09-928-048A-4        Sequence 4, Appli
     4      422    100.0     84  17  US-09-323-606C-1        Sequence 1, Appli
     5      422    100.0     84  20  US-09-636-530-1         Sequence 1, Appli
     6      422    100.0     84  23  US-09-928-047B-5        Sequence 5, Appli
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     7      422    100.0     84  23  US-09-928-048A-3        Sequence 3, Appli
     8      418     99.1     82  17  US-09-323-606C-2        Sequence 2, Appli
     9      418     99.1     82  20  US-09-636-530-4         Sequence 4, Appli
    10      418     99.1     82  23  US-09-928-047B-2        Sequence 2, Appli
    11      417     98.8     83  24  US-10-002-818-2         Sequence 2, Appli
    12      417     98.8     84   1  PCT-US02-21356-1       Sequence 1, Appli
    13      417     98.8     84   1  PCT-US98-20848-1       Sequence 1, Appli
    14      417     98.8     84   3  US-07-806-271-2        Sequence 2, Appli
    15      417     98.8     84   4  US-08-016-171-2        Sequence 2, Appli
    16      417     98.8     84   7  US-08-329-856-2        Sequence 2, Appli
    17      417     98.8     84   7  US-08-345-151A-16      Sequence 16, Appl
    18      417     98.8     84   7  US-08-350-530A-25      Sequence 25, Appl
    19      417     98.8     84   7  US-08-350-709-9        Sequence 9, Appli
    20      417     98.8     84   7  US-08-350-709B-9       Sequence 9, Appli
    21      417     98.8     84   9  US-08-586-768-1        Sequence 1, Appli
    22      417     98.8     84  15  US-09-169-786-1         Sequence 1, Appli
    23      417     98.8     84  15  US-09-169-786-1         Sequence 1, Appli
    24      417     98.8     84  16  US-09-231-422B-2        Sequence 2, Appli
    25      417     98.8     84  16  US-09-231-422D-2        Sequence 2, Appli
    26      417     98.8     84  17  US-09-344-639D-1        Sequence 1, Appli
    27      417     98.8     84  20  US-09-657-276-256       Sequence 256, App
    28      417     98.8     84  22  US-09-843-221A-10       Sequence 10, Appl
    29      417     98.8     84  22  US-09-898-398-1         Sequence 1, Appli
    30      417     98.8     84  24  US-10-002-818-1         Sequence 1, Appli
    31      417     98.8    115  16  US-09-287-332-6         Sequence 6, Appli
    32      417     98.8    115  25  US-10-157-031-50        Sequence 50, Appl
    33      417     98.8    148  21  US-09-760-483-332       Sequence 332, App
    34      417     98.8    148  26  US-10-206-021-473       Sequence 473, App
    35      417     98.8    148  26  US-10-213-073-332       Sequence 332, App
    36      413     97.9     82  17  US-09-344-639D-2        Sequence 2, Appli
    37      412     97.6     84   1  PCT-US94-12205-1       Sequence 1, Appli
    38      412     97.6     84   8  US-08-455-919-1        Sequence 1, Appli
    39      412     97.6     84   8  US-08-458-075-1        Sequence 1, Appli
    40      410     97.2     84   8  US-08-466-487-16       Sequence 16, Appl
    41      409     96.9     80  17  US-09-323-606C-10       Sequence 10, Appl
    42      407     96.4     84  19  US-09-555-447-1         Sequence 1, Appli
    43      407     96.4     84  19  US-09-555-476-1         Sequence 1, Appli
    44      400     94.8     78  17  US-09-323-606C-4        Sequence 4, Appli
    45      400     94.8     78  23  US-09-928-047B-4        Sequence 4, Appli


                                  ALIGNMENTS


RESULT 1
US-09-636-530-2
; Sequence 2, Application US/09636530
; GENERAL INFORMATION:
;  APPLICANT: Cantor, Thomas
;  TITLE OF INVENTION: PARATHYROID HORMONE ANTAGONISTS OR
;  TITLE OF INVENTION:  MODULATORS AND USES THEREFOR
;  FILE REFERENCE: 53221-20003.00
;  CURRENT APPLICATION NUMBER: US/09/636,530
;  CURRENT FILING DATE:  2000-08-10
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 83
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-636-530-2

  Query Match             100.0%;  Score 422;  DB 20;  Length 83;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-42;
  Matches   83;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60

Qy         61 SHEKSLGEANKADVNVLTKAKSQ 83
              |||||||||||||||||||||||
Db         61 SHEKSLGEANKADVNVLTKAKSQ 83
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RESULT 2
US-09-928-047B-1
; Sequence 1, Application US/09928047B
; GENERAL INFORMATION:
;  APPLICANT: Cantor, Thomas
;  TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
;  TITLE OF INVENTION:  ANTAGONIST OR MODULATORS AND OSTEOPOROSIS
;  FILE REFERENCE: 53221-20002.00
;  CURRENT APPLICATION NUMBER: US/09/928,047B
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: US 60/224,446
;  PRIOR FILING DATE: 2000-08-10
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 83
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-928-047B-1

  Query Match             100.0%;  Score 422;  DB 23;  Length 83;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-42;
  Matches   83;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60

Qy         61 SHEKSLGEANKADVNVLTKAKSQ 83
              |||||||||||||||||||||||
Db         61 SHEKSLGEANKADVNVLTKAKSQ 83


RESULT 3
US-09-928-048A-4
; Sequence 4, Application US/09928048A
; GENERAL INFORMATION:
;  APPLICANT: Scantibodies Laboratory, Inc.
;  APPLICANT:  Cantor, Thomas L.
;  TITLE OF INVENTION: METHODS AND DEVICES FOR DIRECT
;  TITLE OF INVENTION:  DETERMINATION OF CYCLASE INHIBITING PARATHYROID HORMONE
;  FILE REFERENCE: 53221-20015.00
;  CURRENT APPLICATION NUMBER: US/09/928,048A
;  CURRENT FILING DATE:  2000-08-10
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 83
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-928-048A-4

  Query Match             100.0%;  Score 422;  DB 23;  Length 83;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-42;
  Matches   83;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60

Qy         61 SHEKSLGEANKADVNVLTKAKSQ 83
              |||||||||||||||||||||||
Db         61 SHEKSLGEANKADVNVLTKAKSQ 83


RESULT 4
US-09-323-606C-1
; Sequence 1, Application US/09323606C
; GENERAL INFORMATION:
;  APPLICANT: Cantor, Thomas
;  TITLE OF INVENTION: PARATHYROID HORMONE ANTAGONISTS OR
;  TITLE OF INVENTION:  MODULATORS AND METHODS THEREFOR
;  FILE REFERENCE: 53221-20009.00
;  CURRENT APPLICATION NUMBER: US/09/323,606C
;  CURRENT FILING DATE:  1999-01-18
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 84
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-323-606C-1

  Query Match             100.0%;  Score 422;  DB 17;  Length 84;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-42;
  Matches   83;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 61

Qy         61 SHEKSLGEANKADVNVLTKAKSQ 83
              |||||||||||||||||||||||
Db         62 SHEKSLGEANKADVNVLTKAKSQ 84


RESULT 5
US-09-636-530-1
; Sequence 1, Application US/09636530
; GENERAL INFORMATION:
;  APPLICANT: Cantor, Thomas
;  TITLE OF INVENTION: PARATHYROID HORMONE ANTAGONISTS OR
;  TITLE OF INVENTION:  MODULATORS AND USES THEREFOR
;  FILE REFERENCE: 53221-20003.00
;  CURRENT APPLICATION NUMBER: US/09/636,530
;  CURRENT FILING DATE:  2000-08-10
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 84
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-636-530-1

  Query Match             100.0%;  Score 422;  DB 20;  Length 84;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-42;
  Matches   83;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 61

Qy         61 SHEKSLGEANKADVNVLTKAKSQ 83
              |||||||||||||||||||||||
Db         62 SHEKSLGEANKADVNVLTKAKSQ 84


RESULT 6
US-09-928-047B-5
; Sequence 5, Application US/09928047B
; GENERAL INFORMATION:
;  APPLICANT: Cantor, Thomas
;  TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
;  TITLE OF INVENTION:  ANTAGONIST OR MODULATORS AND OSTEOPOROSIS
;  FILE REFERENCE: 53221-20002.00
;  CURRENT APPLICATION NUMBER: US/09/928,047B
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: US 60/224,446
;  PRIOR FILING DATE: 2000-08-10
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 84
;   TYPE: PRT
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;   ORGANISM: Homo sapiens
US-09-928-047B-5

  Query Match             100.0%;  Score 422;  DB 23;  Length 84;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-42;
  Matches   83;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 61

Qy       61 SHEKSLGEANKADVNVLTKAKSQ 83
            |||||||||||||||||||||||
Db       62 SHEKSLGEANKADVNVLTKAKSQ 84


RESULT 7
US-09-928-048A-3
; Sequence 3, Application US/09928048A
; GENERAL INFORMATION:
;  APPLICANT: Scantibodies Laboratory, Inc.
;  APPLICANT:  Cantor, Thomas L.
;  TITLE OF INVENTION: METHODS AND DEVICES FOR DIRECT
;  TITLE OF INVENTION:  DETERMINATION OF CYCLASE INHIBITING PARATHYROID HORMONE
;  FILE REFERENCE: 53221-20015.00
;  CURRENT APPLICATION NUMBER: US/09/928,048A
;  CURRENT FILING DATE:  2000-08-10
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 84
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-928-048A-3

  Query Match             100.0%;  Score 422;  DB 23;  Length 84;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-42;
  Matches   83;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 61

Qy       61 SHEKSLGEANKADVNVLTKAKSQ 83
            |||||||||||||||||||||||
Db       62 SHEKSLGEANKADVNVLTKAKSQ 84


RESULT 8
US-09-323-606C-2
; Sequence 2, Application US/09323606C
; GENERAL INFORMATION:
;  APPLICANT: Cantor, Thomas
;  TITLE OF INVENTION: PARATHYROID HORMONE ANTAGONISTS OR
;  TITLE OF INVENTION:  MODULATORS AND METHODS THEREFOR
;  FILE REFERENCE: 53221-20009.00
;  CURRENT APPLICATION NUMBER: US/09/323,606C
;  CURRENT FILING DATE:  1999-01-18
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 82
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-323-606C-2

  Query Match              99.1%;  Score 418;  DB 17;  Length 82;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-42;
  Matches   82;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        2 SEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVES 61
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 SEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVES 60
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```
Qy       62 HEKSLGEANKADVNVLTKAKSQ 83
            ||||||||||||||||||||||
Db       61 HEKSLGEANKADVNVLTKAKSQ 82


RESULT 9
US-09-636-530-4
; Sequence 4, Application US/09636530
; GENERAL INFORMATION:
;  APPLICANT: Cantor, Thomas
;  TITLE OF INVENTION: PARATHYROID HORMONE ANTAGONISTS OR
;  TITLE OF INVENTION:  MODULATORS AND USES THEREFOR
;  FILE REFERENCE: 53221-20003.00
;  CURRENT APPLICATION NUMBER: US/09/636,530
;  CURRENT FILING DATE:  2000-08-10
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 82
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-636-530-4

  Query Match              99.1%;  Score 418;  DB 20;  Length 82;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-42;
  Matches   82;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        2 SEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVES 61
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 SEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVES 60

Qy       62 HEKSLGEANKADVNVLTKAKSQ 83
            ||||||||||||||||||||||
Db       61 HEKSLGEANKADVNVLTKAKSQ 82


RESULT 10
US-09-928-047B-2
; Sequence 2, Application US/09928047B
; GENERAL INFORMATION:
;  APPLICANT: Cantor, Thomas
;  TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
;  TITLE OF INVENTION:  ANTAGONIST OR MODULATORS AND OSTEOPOROSIS
;  FILE REFERENCE: 53221-20002.00
;  CURRENT APPLICATION NUMBER: US/09/928,047B
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: US 60/224,446
;  PRIOR FILING DATE: 2000-08-10
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 82
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-928-047B-2

  Query Match              99.1%;  Score 418;  DB 23;  Length 82;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-42;
  Matches   82;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        2 SEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVES 61
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 SEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVES 60

Qy       62 HEKSLGEANKADVNVLTKAKSQ 83
            ||||||||||||||||||||||
Db       61 HEKSLGEANKADVNVLTKAKSQ 82


RESULT 11
US-10-002-818-2
; Sequence 2, Application US/10002818
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; GENERAL INFORMATION:
;  APPLICANT: Cantor, Thomas L.
;  TITLE OF INVENTION: Methods for Monitoring Therapeutic Suppression of Parathyroid Hor
;  TITLE OF INVENTION:  Renal Patients Having Secondary Hyperparathyroidism
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/10/002,818
;  CURRENT FILING DATE:  2001-11-02
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: Microsoft Word 2000 - ASCII format
; SEQ ID NO 2
;   LENGTH: 83
;   TYPE: PRT
;   ORGANISM: human parathyroid hormone peptide fragment
US-10-002-818-2

  Query Match             98.8%;  Score 417;  DB 24;  Length 83;
  Best Local Similarity   98.8%;  Pred. No. 6.5e-42;
  Matches   82;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60

Qy      61 SHEKSLGEANKADVNVLTKAKSQ 83
             |||||||||:|||||||||||||
Db      61 SHEKSLGEADKADVNVLTKAKSQ 83


RESULT 12
PCT-US02-21356-1
; Sequence 1, Application PC/TUS0221356
; GENERAL INFORMATION:
;  APPLICANT: Hutchison, James Scott
;  TITLE OF INVENTION: PARATHYROID HORMONE ANTIBODIES AND RELATED METHODS
;  FILE REFERENCE: A1713
;  CURRENT APPLICATION NUMBER: PCT/US02/21356
;  CURRENT FILING DATE:  2002-07-03
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 84
;   TYPE: PRT
;   ORGANISM: Homo sapiens
PCT-US02-21356-1

  Query Match             98.8%;  Score 417;  DB 1;  Length 84;
  Best Local Similarity   98.8%;  Pred. No. 6.6e-42;
  Matches   82;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 61

Qy      61 SHEKSLGEANKADVNVLTKAKSQ 83
             |||||||||:|||||||||||||
Db      62 SHEKSLGEADKADVNVLTKAKSQ 84


RESULT 13
PCT-US98-20848-1
; Sequence 1, Application PC/TUS9820848A
; GENERAL INFORMATION:
;  APPLICANT: Sato, Masahiko
;  TITLE OF INVENTION: Method of Building and Maintaining Bone
;  FILE REFERENCE: X-11480
;  CURRENT APPLICATION NUMBER: PCT/US98/20848A
;  CURRENT FILING DATE: 1998-10-05
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 84
;   TYPE: PRT
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: Description of Unknown Organism:Human
PCT-US98-20848-1

  Query Match             98.8%;  Score 417;  DB 1;  Length 84;
  Best Local Similarity   98.8%;  Pred. No. 6.6e-42;
  Matches   82;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 61

Qy      61 SHEKSLGEANKADVNVLTKAKSQ 83
             |||||||||:|||||||||||||
Db      62 SHEKSLGEADKADVNVLTKAKSQ 84


RESULT 14
US-07-806-271-2
; Sequence 2, Application US/07806271
;  GENERAL INFORMATION:
;    APPLICANT:  BOZZATO, Richard P.
;    APPLICANT:  KRONIS, K. Anne
;    TITLE OF INVENTION:  OXIDATION RESISTANT VARIANTS OF
;    TITLE OF INVENTION:  PARATHYROID HORMONE
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  1800 Diagonal Road, Suite 500
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  USA
;      ZIP:  22313-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/806,271
;      FILING DATE:  19911213
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  16777/156 ALLE
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)836-9300
;      TELEFAX:  (703)683-4109
;      TELEX:  899149
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  84 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-07-806-271-2

  Query Match             98.8%;  Score 417;  DB 3;  Length 84;
  Best Local Similarity   98.8%;  Pred. No. 6.6e-42;
  Matches   82;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 61

Qy      61 SHEKSLGEANKADVNVLTKAKSQ 83
             |||||||||:|||||||||||||
Db      62 SHEKSLGEADKADVNVLTKAKSQ 84


RESULT 15
US-08-016-171-2
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; Sequence 2, Application US/08016171
;  GENERAL INFORMATION:
;    APPLICANT:  FUKUDA, Tsunehiko
;    APPLICANT:  OSHIKA, Yuri
;    APPLICANT:  YAMADA, Takao
;    TITLE OF INVENTION:  SYNTHETIC GENE CODING FOR HUMAN
;    TITLE OF INVENTION:  PARATHYROID HORMONE
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
;      ADDRESSEE:  CUSHMAN
;      STREET:  130 Water Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  US
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/016,171
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/765,371
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WILLIAMS, Gregory D
;      REGISTRATION NUMBER:  30,901
;      REFERENCE/DOCKET NUMBER:  41,288
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)523-3400
;      TELEFAX:  (617)523-6440
;      TELEX:  200291 STRE UR
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  84 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-016-171-2

  Query Match             98.8%;  Score 417;  DB 4;  Length 84;
  Best Local Similarity   98.8%;  Pred. No. 6.6e-42;
  Matches   82;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 61

Qy         61 SHEKSLGEANKADVNVLTKAKSQ 83
                |||||||||:|||||||||||||
Db         62 SHEKSLGEADKADVNVLTKAKSQ 84


Search completed: March 13, 2003, 14:57:47
Job time : 177.53 secs
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                    GenCore version 5.1.4_p5_4578
              Copyright (c) 1993 - 2003  Compugen Ltd.

OM protein - protein search, using sw model

Run on:        March 13, 2003, 14:49:19 ; Search time 29.7313 Seconds
                                          (without alignments)
                                          362.927 Million cell updates/sec

Title:         US-09-636-530-2
Perfect score: 422
Sequence:      1 VSEIQLMHNLGKHLNSMERV..........KSLGEANKADVNVLTKAKSQ 83

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:      596842 seqs, 130003698 residues

Total number of hits satisfying chosen parameters:      596842

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Pending_Patents_AA_New:*
               1:  /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*
               2:  /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
               3:  /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
               4:  /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
               5:  /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
               6:  /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*
               7:  /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                SUMMARIES
                  %
Result          Query
  No.   Score   Match Length DB  ID                        Description
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    1     422   100.0     84  1  PCT-US02-25348-1           Sequence 1, Appli
    2     422   100.0     84  5  US-09-231-422F-2           Sequence 2, Appli
    3     422   100.0     84  6  US-10-215-770-1            Sequence 1, Appli
    4     417    98.8     84  1  PCT-US02-40891-505         Sequence 505, App
    5     417    98.8     84  1  PCT-US02-40891-508         Sequence 508, App
    6     417    98.8     84  1  PCT-US02-40891-530         Sequence 530, App
    7     417    98.8     84  1  PCT-US02-40891-531         Sequence 531, App
    8     417    98.8     84  1  PCT-US02-40891-532         Sequence 532, App
    9     417    98.8     84  1  PCT-US02-40891-626         Sequence 626, App
   10     417    98.8     84  1  PCT-US03-02155-13          Sequence 13, Appl
   11     417    98.8     84  5  US-09-383-590-1            Sequence 1, Appli
   12     417    98.8     84  6  US-10-224-522-1            Sequence 1, Appli
   13     417    98.8     84  6  US-10-311-366-10           Sequence 10, Appl
   14     417    98.8    692  1  PCT-US02-40891-289         Sequence 289, App
   15     417    98.8    692  1  PCT-US02-40891-292         Sequence 292, App
   16     417    98.8    693  1  PCT-US02-40891-314         Sequence 314, App
   17     417    98.8    693  1  PCT-US02-40891-315         Sequence 315, App
   18     417    98.8    693  1  PCT-US02-40891-316         Sequence 316, App
   19     417    98.8    693  1  PCT-US02-40891-410         Sequence 410, App
   20     400    94.8     78  5  US-09-231-422F-6           Sequence 6, Appli
   21     366    86.7     84  1  PCT-US02-25348-3           Sequence 3, Appli
   22     366    86.7     84  6  US-10-215-770-3            Sequence 3, Appli
   23     359    85.1     84  1  PCT-US02-25348-4           Sequence 4, Appli
   24     359    85.1     84  6  US-10-311-366-2            Sequence 2, Appli
   25     359    85.1     84  6  US-10-215-770-4            Sequence 4, Appli
   26     355    84.1     84  1  PCT-US02-25348-2           Sequence 2, Appli
   27     355    84.1     84  6  US-10-215-770-2            Sequence 2, Appli
   28     315    74.6     84  6  US-10-311-366-11           Sequence 11, Appl
   29     311    73.7     84  1  PCT-US02-25348-5           Sequence 5, Appli
   30     311    73.7     84  6  US-10-215-770-5            Sequence 5, Appli
   31     253    60.0     91  7  US-60-443-566-2959         Sequence 2959, Ap
   32     253    60.0    123  7  US-60-443-566-2960         Sequence 2960, Ap
   33     224    53.1     44  6  US-10-311-366-19           Sequence 19, Appl
   34     193    45.7     38  6  US-10-311-366-18           Sequence 18, Appl
   35   184.5    43.7    671  1  PCT-US02-40891-1199        Sequence 1199, Ap
   36   184.5    43.7    671  1  PCT-US02-40891-1554        Sequence 1554, Ap
   37     183    43.4    640  1  PCT-US02-40891-280         Sequence 280, App
   38     183    43.4    640  1  PCT-US02-40891-288         Sequence 288, App
   39     183    43.4    640  1  PCT-US02-40891-1602        Sequence 1602, Ap
   40     183    43.4    640  1  PCT-US02-40891-1603        Sequence 1603, Ap
   41     183    43.4    643  1  PCT-US02-40891-241         Sequence 241, App
   42   181.5    43.0    642  1  PCT-US02-40891-276         Sequence 276, App
   43     178    42.2    643  1  PCT-US02-40891-267         Sequence 267, App
   44     175    41.5     34  1  PCT-US02-40891-456         Sequence 456, App
   45     175    41.5     34  1  PCT-US02-40891-457         Sequence 457, App


                                 ALIGNMENTS


RESULT 1
PCT-US02-25348-1
; Sequence 1, Application PC/TUS0225348
; GENERAL INFORMATION:
;  APPLICANT: Cantor, Thomas L.
;  TITLE OF INVENTION: PARATHYROID HORMONE ANTAGONISTS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 53221-20002.40
;  CURRENT APPLICATION NUMBER: PCT/US02/25348
;  CURRENT FILING DATE:  2002-08-09
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 84
;   TYPE: PRT
;   ORGANISM: Homo sapiens
PCT-US02-25348-1

  Query Match             100.0%;  Score 422;  DB 1;  Length 84;
  Best Local Similarity   100.0%;  Pred. No. 5.4e-40;
  Matches   83;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 61

Qy         61 SHEKSLGEANKADVNVLTKAKSQ 83
              |||||||||||||||||||||||
Db         62 SHEKSLGEANKADVNVLTKAKSQ 84


RESULT 2
US-09-231-422F-2
; Sequence 2, Application US/09231422F
; GENERAL INFORMATION:
;  APPLICANT: Scantibodies Laboratory, Inc.
;  APPLICANT:  Cantor, Thomas
;  APPLICANT:  Gao, Ping
;  TITLE OF INVENTION: METHODS, KITS AND ANTIBODIES FOR DETECTING
;  TITLE OF INVENTION:  PARATHYROID HORMONE
;  FILE REFERENCE: 53221-20006.00
;  CURRENT APPLICATION NUMBER: US/09/231,422F
;  CURRENT FILING DATE:  1999-01-14
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 84
;   TYPE: PRT
;   ORGANISM: Homo sapiens
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US-09-231-422F-2

  Query Match             100.0%;  Score 422;  DB 5;  Length 84;
  Best Local Similarity   100.0%;  Pred. No. 5.4e-40;
  Matches   83;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 61

Qy         61 SHEKSLGEANKADVNVLTKAKSQ 83
              |||||||||||||||||||||||
Db         62 SHEKSLGEANKADVNVLTKAKSQ 84


RESULT 3
US-10-215-770-1
; Sequence 1, Application US/10215770
; GENERAL INFORMATION:
;  APPLICANT: Cantor, Thomas L.
;  TITLE OF INVENTION: PARATHYROID HORMONE ANTAGONISTS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 53221-20002.20
;  CURRENT APPLICATION NUMBER: US/10/215,770
;  CURRENT FILING DATE:  2002-12-16
;  PRIOR APPLICATION NUMBER: US 60/224,446
;  PRIOR FILING DATE: 2000-08-10
;  PRIOR APPLICATION NUMBER: US 60/224,447
;  PRIOR FILING DATE: 2000-08-10
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 84
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-215-770-1

  Query Match             100.0%;  Score 422;  DB 6;  Length 84;
  Best Local Similarity   100.0%;  Pred. No. 5.4e-40;
  Matches   83;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 61

Qy         61 SHEKSLGEANKADVNVLTKAKSQ 83
              |||||||||||||||||||||||
Db         62 SHEKSLGEANKADVNVLTKAKSQ 84


RESULT 4
PCT-US02-40891-505
; Sequence 505, Application PC/TUS0240891
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc.
;  TITLE OF INVENTION: Albumin Fusion Proteins
;  FILE REFERENCE: PF564PCT
;  CURRENT APPLICATION NUMBER: PCT/US02/40891
;  CURRENT FILING DATE:  2002-12-23
;  PRIOR APPLICATION NUMBER: 60/341,811
;  PRIOR FILING DATE: 2001-12-21
;  PRIOR APPLICATION NUMBER: 60/360,000
;  PRIOR FILING DATE: 2002-02-28
;  PRIOR APPLICATION NUMBER: 60/378,950
;  PRIOR FILING DATE: 2002-05-10
;  PRIOR APPLICATION NUMBER: 60/398,008
;  PRIOR FILING DATE: 2002-07-24
;  PRIOR APPLICATION NUMBER: 60/411,355
;  PRIOR FILING DATE: 2002-09-18
;  PRIOR APPLICATION NUMBER: 60/414,984
;  PRIOR FILING DATE: 2002-10-02
;  PRIOR APPLICATION NUMBER: 60/417,611
;  PRIOR FILING DATE: 2002-10-11
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;  PRIOR APPLICATION NUMBER: 60/420,246
;  PRIOR FILING DATE: 2002-10-23
;  PRIOR APPLICATION NUMBER: 60/423,623
;  PRIOR FILING DATE: 2002-11-05
;  PRIOR APPLICATION NUMBER: 60/351,360
;  PRIOR FILING DATE: 2002-01-28
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 2222
;  SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 505
;   LENGTH: 84
;   TYPE: PRT
;   ORGANISM: Homo sapiens
PCT-US02-40891-505

  Query Match             98.8%;  Score 417;  DB 1;  Length 84;
  Best Local Similarity   98.8%;  Pred. No. 2e-39;
  Matches   82;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 61

Qy         61 SHEKSLGEANKADVNVLTKAKSQ 83
              |||||||||:|||||||||||||
Db         62 SHEKSLGEADKADVNVLTKAKSQ 84


RESULT 5
PCT-US02-40891-508
; Sequence 508, Application PC/TUS0240891
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc.
;  TITLE OF INVENTION: Albumin Fusion Proteins
;  FILE REFERENCE: PF564PCT
;  CURRENT APPLICATION NUMBER: PCT/US02/40891
;  CURRENT FILING DATE:  2002-12-23
;  PRIOR APPLICATION NUMBER: 60/341,811
;  PRIOR FILING DATE: 2001-12-21
;  PRIOR APPLICATION NUMBER: 60/360,000
;  PRIOR FILING DATE: 2002-02-28
;  PRIOR APPLICATION NUMBER: 60/378,950
;  PRIOR FILING DATE: 2002-05-10
;  PRIOR APPLICATION NUMBER: 60/398,008
;  PRIOR FILING DATE: 2002-07-24
;  PRIOR APPLICATION NUMBER: 60/411,355
;  PRIOR FILING DATE: 2002-09-18
;  PRIOR APPLICATION NUMBER: 60/414,984
;  PRIOR FILING DATE: 2002-10-02
;  PRIOR APPLICATION NUMBER: 60/417,611
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/420,246
;  PRIOR FILING DATE: 2002-10-23
;  PRIOR APPLICATION NUMBER: 60/423,623
;  PRIOR FILING DATE: 2002-11-05
;  PRIOR APPLICATION NUMBER: 60/351,360
;  PRIOR FILING DATE: 2002-01-28
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 2222
;  SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 508
;   LENGTH: 84
;   TYPE: PRT
;   ORGANISM: Homo sapiens
PCT-US02-40891-508

  Query Match             98.8%;  Score 417;  DB 1;  Length 84;
  Best Local Similarity   98.8%;  Pred. No. 2e-39;
  Matches   82;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 61
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Qy     61 SHEKSLGEANKADVNVLTKAKSQ 83
          |||||||||:|||||||||||||
Db     62 SHEKSLGEADKADVNVLTKAKSQ 84


RESULT 6
PCT-US02-40891-530
; Sequence 530, Application PC/TUS0240891
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc.
;  TITLE OF INVENTION: Albumin Fusion Proteins
;  FILE REFERENCE: PF564PCT
;  CURRENT APPLICATION NUMBER: PCT/US02/40891
;  CURRENT FILING DATE:  2002-12-23
;  PRIOR APPLICATION NUMBER: 60/341,811
;  PRIOR FILING DATE: 2001-12-21
;  PRIOR APPLICATION NUMBER: 60/360,000
;  PRIOR FILING DATE: 2002-02-28
;  PRIOR APPLICATION NUMBER: 60/378,950
;  PRIOR FILING DATE: 2002-05-10
;  PRIOR APPLICATION NUMBER: 60/398,008
;  PRIOR FILING DATE: 2002-07-24
;  PRIOR APPLICATION NUMBER: 60/411,355
;  PRIOR FILING DATE: 2002-09-18
;  PRIOR APPLICATION NUMBER: 60/414,984
;  PRIOR FILING DATE: 2002-10-02
;  PRIOR APPLICATION NUMBER: 60/417,611
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/420,246
;  PRIOR FILING DATE: 2002-10-23
;  PRIOR APPLICATION NUMBER: 60/423,623
;  PRIOR FILING DATE: 2002-11-05
;  PRIOR APPLICATION NUMBER: 60/351,360
;  PRIOR FILING DATE: 2002-01-28
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 2222
;  SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 530
;   LENGTH: 84
;   TYPE: PRT
;   ORGANISM: Homo sapiens
PCT-US02-40891-530

  Query Match             98.8%;  Score 417;  DB 1;  Length 84;
  Best Local Similarity   98.8%;  Pred. No. 2e-39;
  Matches   82;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 61

Qy     61 SHEKSLGEANKADVNVLTKAKSQ 83
          |||||||||:|||||||||||||
Db     62 SHEKSLGEADKADVNVLTKAKSQ 84


RESULT 7
PCT-US02-40891-531
; Sequence 531, Application PC/TUS0240891
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc.
;  TITLE OF INVENTION: Albumin Fusion Proteins
;  FILE REFERENCE: PF564PCT
;  CURRENT APPLICATION NUMBER: PCT/US02/40891
;  CURRENT FILING DATE:  2002-12-23
;  PRIOR APPLICATION NUMBER: 60/341,811
;  PRIOR FILING DATE: 2001-12-21
;  PRIOR APPLICATION NUMBER: 60/360,000
;  PRIOR FILING DATE: 2002-02-28
;  PRIOR APPLICATION NUMBER: 60/378,950
;  PRIOR FILING DATE: 2002-05-10
;  PRIOR APPLICATION NUMBER: 60/398,008
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;  PRIOR FILING DATE: 2002-07-24
;  PRIOR APPLICATION NUMBER: 60/411,355
;  PRIOR FILING DATE: 2002-09-18
;  PRIOR APPLICATION NUMBER: 60/414,984
;  PRIOR FILING DATE: 2002-10-02
;  PRIOR APPLICATION NUMBER: 60/417,611
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/420,246
;  PRIOR FILING DATE: 2002-10-23
;  PRIOR APPLICATION NUMBER: 60/423,623
;  PRIOR FILING DATE: 2002-11-05
;  PRIOR APPLICATION NUMBER: 60/351,360
;  PRIOR FILING DATE: 2002-01-28
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 2222
;  SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 531
;   LENGTH: 84
;   TYPE: PRT
;   ORGANISM: Homo sapiens
PCT-US02-40891-531

  Query Match             98.8%;  Score 417;  DB 1;  Length 84;
  Best Local Similarity   98.8%;  Pred. No. 2e-39;
  Matches   82;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 61

Qy     61 SHEKSLGEANKADVNVLTKAKSQ 83
          |||||||||:|||||||||||||
Db     62 SHEKSLGEADKADVNVLTKAKSQ 84


RESULT 8
PCT-US02-40891-532
; Sequence 532, Application PC/TUS0240891
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc.
;  TITLE OF INVENTION: Albumin Fusion Proteins
;  FILE REFERENCE: PF564PCT
;  CURRENT APPLICATION NUMBER: PCT/US02/40891
;  CURRENT FILING DATE:  2002-12-23
;  PRIOR APPLICATION NUMBER: 60/341,811
;  PRIOR FILING DATE: 2001-12-21
;  PRIOR APPLICATION NUMBER: 60/360,000
;  PRIOR FILING DATE: 2002-02-28
;  PRIOR APPLICATION NUMBER: 60/378,950
;  PRIOR FILING DATE: 2002-05-10
;  PRIOR APPLICATION NUMBER: 60/398,008
;  PRIOR FILING DATE: 2002-07-24
;  PRIOR APPLICATION NUMBER: 60/411,355
;  PRIOR FILING DATE: 2002-09-18
;  PRIOR APPLICATION NUMBER: 60/414,984
;  PRIOR FILING DATE: 2002-10-02
;  PRIOR APPLICATION NUMBER: 60/417,611
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/420,246
;  PRIOR FILING DATE: 2002-10-23
;  PRIOR APPLICATION NUMBER: 60/423,623
;  PRIOR FILING DATE: 2002-11-05
;  PRIOR APPLICATION NUMBER: 60/351,360
;  PRIOR FILING DATE: 2002-01-28
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 2222
;  SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 532
;   LENGTH: 84
;   TYPE: PRT
;   ORGANISM: Homo sapiens
PCT-US02-40891-532
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  Best Local Similarity   98.8%;  Pred. No. 2e-39;
  Matches   82;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 61

Qy     61 SHEKSLGEANKADVNVLTKAKSQ 83
          |||||||||:|||||||||||||
Db     62 SHEKSLGEADKADVNVLTKAKSQ 84


RESULT 9
PCT-US02-40891-626
; Sequence 626, Application PC/TUS0240891
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc.
;  TITLE OF INVENTION: Albumin Fusion Proteins
;  FILE REFERENCE: PF564PCT
;  CURRENT APPLICATION NUMBER: PCT/US02/40891
;  CURRENT FILING DATE:  2002-12-23
;  PRIOR APPLICATION NUMBER: 60/341,811
;  PRIOR FILING DATE: 2001-12-21
;  PRIOR APPLICATION NUMBER: 60/360,000
;  PRIOR FILING DATE: 2002-02-28
;  PRIOR APPLICATION NUMBER: 60/378,950
;  PRIOR FILING DATE: 2002-05-10
;  PRIOR APPLICATION NUMBER: 60/398,008
;  PRIOR FILING DATE: 2002-07-24
;  PRIOR APPLICATION NUMBER: 60/411,355
;  PRIOR FILING DATE: 2002-09-18
;  PRIOR APPLICATION NUMBER: 60/414,984
;  PRIOR FILING DATE: 2002-10-02
;  PRIOR APPLICATION NUMBER: 60/417,611
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/420,246
;  PRIOR FILING DATE: 2002-10-23
;  PRIOR APPLICATION NUMBER: 60/423,623
;  PRIOR FILING DATE: 2002-11-05
;  PRIOR APPLICATION NUMBER: 60/351,360
;  PRIOR FILING DATE: 2002-01-28
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 2222
;  SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 626
;   LENGTH: 84
;   TYPE: PRT
;   ORGANISM: Homo sapiens
PCT-US02-40891-626

  Query Match             98.8%;  Score 417;  DB 1;  Length 84;
  Best Local Similarity   98.8%;  Pred. No. 2e-39;
  Matches   82;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 61

Qy     61 SHEKSLGEANKADVNVLTKAKSQ 83
          |||||||||:|||||||||||||
Db     62 SHEKSLGEADKADVNVLTKAKSQ 84


RESULT 10
PCT-US03-02155-13
; Sequence 13, Application PC/TUS0302155
; GENERAL INFORMATION:
;  APPLICANT: Gardella, Thomas J.
;  APPLICANT:  Kronenberg, Henry M.
;  APPLICANT:  Potts, John T.
;  TITLE OF INVENTION: Conformationally Constrained Parathyroid Hormone (PTH) Analogs
;  TITLE OF INVENTION:  With Lactam Bridges
;  FILE REFERENCE: 0609.514PC00
;  CURRENT APPLICATION NUMBER: PCT/US03/02155
;  CURRENT FILING DATE:  2003-01-24
;  NUMBER OF SEQ ID NOS: 37
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
;   LENGTH: 84
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (84)..(84)
;   OTHER INFORMATION: AMIDATION
PCT-US03-02155-13

  Query Match             98.8%;  Score 417;  DB 1;  Length 84;
  Best Local Similarity   98.8%;  Pred. No. 2e-39;
  Matches   82;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 61

Qy     61 SHEKSLGEANKADVNVLTKAKSQ 83
          |||||||||:|||||||||||||
Db     62 SHEKSLGEADKADVNVLTKAKSQ 84


RESULT 11
US-09-383-590-1
; Sequence 1, Application US/09383590
; GENERAL INFORMATION:
;  APPLICANT: Backstrom, Kjell G. E.
;  APPLICANT:  Wallmark, Bjorn
;  APPLICANT:  Dahlback, Magnus
;  APPLICANT:  Edman, Peter
;  APPLICANT:  Johansson, Ann
;  TITLE OF INVENTION: THERAPEUTIC PREPARATIONS FOR INHALATION
;  FILE REFERENCE: 06275-110002
;  CURRENT APPLICATION NUMBER: US/09/383,590
;  CURRENT FILING DATE:  1999-08-26
;  PRIOR APPLICATION NUMBER: US 08/586,768
;  PRIOR FILING DATE: 1996-01-30
;  PRIOR APPLICATION NUMBER: PCT/SE95/01475
;  PRIOR FILING DATE: 1995-12-08
;  PRIOR APPLICATION NUMBER: SE 9404449-2
;  PRIOR FILING DATE: 1994-12-22
;  PRIOR APPLICATION NUMBER: SE 9502576-3
;  PRIOR FILING DATE: 1995-07-12
;  NUMBER OF SEQ ID NOS: 1
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 84
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-383-590-1

  Query Match             98.8%;  Score 417;  DB 5;  Length 84;
  Best Local Similarity   98.8%;  Pred. No. 2e-39;
  Matches   82;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 61

Qy     61 SHEKSLGEANKADVNVLTKAKSQ 83
          |||||||||:|||||||||||||
Db     62 SHEKSLGEADKADVNVLTKAKSQ 84


RESULT 12
US-10-224-522-1
; Sequence 1, Application US/10224522
```

```
; GENERAL INFORMATION:
;  APPLICANT: Backstrom, Kjell G. E.
;  APPLICANT:  Wallmark, Bjorn
;  APPLICANT:  Dahlbck, Magnus
;  APPLICANT:  Edman, Peter
;  APPLICANT:  Johansson, Ann
;  TITLE OF INVENTION: THERAPEUTIC PREPARATIONS FOR INHALATION
;  FILE REFERENCE: 06275-110003
;  CURRENT APPLICATION NUMBER: US/10/224,522
;  CURRENT FILING DATE:  2002-08-19
;  PRIOR APPLICATION NUMBER: US 09/383,590
;  PRIOR FILING DATE: 1999-08-26
;  PRIOR APPLICATION NUMBER: US 08/586,768
;  PRIOR FILING DATE: 1996-01-30
;  PRIOR APPLICATION NUMBER: PCT/SE95/01475
;  PRIOR FILING DATE: 1995-12-08
;  PRIOR APPLICATION NUMBER: SE 9404449-2
;  PRIOR FILING DATE: 1994-12-22
;  PRIOR APPLICATION NUMBER: SE 9502576-3
;  PRIOR FILING DATE: 1995-07-12
;  NUMBER OF SEQ ID NOS: 1
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 84
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-224-522-1

  Query Match             98.8%;  Score 417;  DB 6;  Length 84;
  Best Local Similarity   98.8%;  Pred. No. 2e-39;
  Matches   82;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy      61 SHEKSLGEANKADVNVLTKAKSQ 83
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Db      62 SHEKSLGEADKADVNVLTKAKSQ 84


RESULT 13
US-10-311-366-10
; Sequence 10, Application US/10311366
; GENERAL INFORMATION:
;  APPLICANT: Holick, Michael F.
;  TITLE OF INVENTION: Regulation Of Cell Proliferation And Differentiation Using Topica
;  TITLE OF INVENTION:  Applied Peptides
;  FILE REFERENCE: 1539.0310001
;  CURRENT APPLICATION NUMBER: US/10/311,366
;  CURRENT FILING DATE:  2002-12-16
;  PRIOR APPLICATION NUMBER: PCT/US01/19650
;  PRIOR FILING DATE: 2001-06-20
;  PRIOR APPLICATION NUMBER: US 60/213,247
;  PRIOR FILING DATE: 2000-06-22
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
;   LENGTH: 84
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: hPTH
US-10-311-366-10

  Query Match             98.8%;  Score 417;  DB 6;  Length 84;
  Best Local Similarity   98.8%;  Pred. No. 2e-39;
  Matches   82;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
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Db       2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 61

Qy      61 SHEKSLGEANKADVNVLTKAKSQ 83
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Db      62 SHEKSLGEADKADVNVLTKAKSQ 84


RESULT 14
PCT-US02-40891-289
; Sequence 289, Application PC/TUS0240891
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc.
;  TITLE OF INVENTION: Albumin Fusion Proteins
;  FILE REFERENCE: PF564PCT
;  CURRENT APPLICATION NUMBER: PCT/US02/40891
;  CURRENT FILING DATE:  2002-12-23
;  PRIOR APPLICATION NUMBER: 60/341,811
;  PRIOR FILING DATE: 2001-12-21
;  PRIOR APPLICATION NUMBER: 60/360,000
;  PRIOR FILING DATE: 2002-02-28
;  PRIOR APPLICATION NUMBER: 60/378,950
;  PRIOR FILING DATE: 2002-05-10
;  PRIOR APPLICATION NUMBER: 60/398,008
;  PRIOR FILING DATE: 2002-07-24
;  PRIOR APPLICATION NUMBER: 60/411,355
;  PRIOR FILING DATE: 2002-09-18
;  PRIOR APPLICATION NUMBER: 60/414,984
;  PRIOR FILING DATE: 2002-10-02
;  PRIOR APPLICATION NUMBER: 60/417,611
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/420,246
;  PRIOR FILING DATE: 2002-10-23
;  PRIOR APPLICATION NUMBER: 60/423,623
;  PRIOR FILING DATE: 2002-11-05
;  PRIOR APPLICATION NUMBER: 60/351,360
;  PRIOR FILING DATE: 2002-01-28
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 2222
;  SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 289
;   LENGTH: 692
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (532)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
PCT-US02-40891-289

  Query Match             98.8%;  Score 417;  DB 1;  Length 692;
  Best Local Similarity   98.8%;  Pred. No. 2.5e-38;
  Matches   82;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
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Qy      61 SHEKSLGEANKADVNVLTKAKSQ 83
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Db     670 SHEKSLGEADKADVNVLTKAKSQ 692


RESULT 15
PCT-US02-40891-292
; Sequence 292, Application PC/TUS0240891
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc.
;  TITLE OF INVENTION: Albumin Fusion Proteins
;  FILE REFERENCE: PF564PCT
;  CURRENT APPLICATION NUMBER: PCT/US02/40891
;  CURRENT FILING DATE:  2002-12-23
;  PRIOR APPLICATION NUMBER: 60/341,811
;  PRIOR FILING DATE: 2001-12-21
;  PRIOR APPLICATION NUMBER: 60/360,000
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;  PRIOR FILING DATE: 2002-02-28
;  PRIOR APPLICATION NUMBER: 60/378,950
;  PRIOR FILING DATE: 2002-05-10
;  PRIOR APPLICATION NUMBER: 60/398,008
;  PRIOR FILING DATE: 2002-07-24
;  PRIOR APPLICATION NUMBER: 60/411,355
;  PRIOR FILING DATE: 2002-09-18
;  PRIOR APPLICATION NUMBER: 60/414,984
;  PRIOR FILING DATE: 2002-10-02
;  PRIOR APPLICATION NUMBER: 60/417,611
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/420,246
;  PRIOR FILING DATE: 2002-10-23
;  PRIOR APPLICATION NUMBER: 60/423,623
;  PRIOR FILING DATE: 2002-11-05
;  PRIOR APPLICATION NUMBER: 60/351,360
;  PRIOR FILING DATE: 2002-01-28
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 2222
;  SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 292
;   LENGTH: 692
;   TYPE: PRT
;   ORGANISM: Homo sapiens
PCT-US02-40891-292

  Query Match             98.8%;  Score 417;  DB 1;  Length 692;
  Best Local Similarity   98.8%;  Pred. No. 2.5e-38;
  Matches   82;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPRKKEDNVLVE 60
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Qy         61 SHEKSLGEANKADVNVLTKAKSQ 83
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Db         83 SHEKSLGEADKADVNVLTKAKSQ 105


Search completed: March 13, 2003, 14:58:43
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